Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                 Copyright
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- protein search, using sw model OM protein

Run on:

; Search time 40 Seconds
 (without alignments)
 584.517 Million cell update 2005, 06:34:51 3, June

tes/sec

243

... NEHLIDMDHEASFFGAFLVG

281 US-10-662-431-2_COPY_39_21 1287 1 TNBLKQMQDKYSKSGIACFL... Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

residues 283416 segs, 96216763 Searched:

125689 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* 4 0 6 4

a rinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

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RESULT 2
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.;
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabb

hypothetical prote sAM-dependent meth conserved hypothet formate dehydrogen hypothetical prote chitin synthase (E hypothetical prote conserved hypothet limpor hypothetical prote ox40 ligand pr	factor beta precursor - pig scrofa domestica (domestic pig)1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 Muschrich, C.; Peterhans, E.; Pauli, U. Jordine Lumor necrosis factor rencoding genes: sequence and comparative anaimater: S17289; MUID:91340150; PMID:187444
A99014 A99387 I40422 H64336 T21543 D45188 T37839 C81749 D90593 H81292 JE0351 S53800 A81896 T28300	factor beta precursor - pig scrofa domestica (domestic pig) -1999 #sequence_revision 10-Sep- 17289 Wuethrich, C.; Peterhans, E.; P 178, 1991 orcine tumor necrosis factor-enc mber: \$17289; MUID:91340150; PMI 17289 c: DNA 204 <kuh> 17289 tumor necrosis factor tokine; cytotoxin; glycoprotein; signal sequence #status predict ct: tumor necrosis factor beta # 10.5%; Score 134.5; imilarity 24.7%; Pred. No. 0. ; Conservative 31; Mismatche STVQEKQONISPLVKERGPQRVAAHITG SAAQPAHQH-PPKHLARGTLKPAAHLVGDPST WESSRSGHSFLSNLHLRNGELVIHEKGFYYIY TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQ TS-YPDFILLMKSARNSCWSKDAEYGLYSIYQ SSQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQ SFFGAF 240 VFFGAF 202</kuh>
100100000000000	ecursor ca (dom _revisi Peterh crosis UID:913 e #stat sis fac sis fac 7%; Pr 7%; Pr 1 : ARGTLKP LRNGELV : ARGTLKP LRNGELV : LSNNSLL SVCPGPQ
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A, Status: preliminary; translated fr
A, Molecule type: DNA
A, Residues: 1-235 < RES >
A, Cross-references: UNIPROT: P36939;
C, Genetics:
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                                                                                                                                                                A;Reference number: A25451
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Residues: 1-234 <IT2>
A;Residues: 1-234 <IT2>
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserter show, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedosp Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the A;Title: Structural analysis of the rabbit FMID:2249779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokin
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted
                                                                                                                                               tumor necrosis
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GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484
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                                                                                                       S.; Todd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 234;
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID: 91016861; PMID: 2216741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                  A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumos A;Reference number: A25451; MUID:86219712; PMID:3519138
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A; Reference number: A25454; MUID:86219711; PMID:3519137
A; Accession: A25454
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Pred. No. 0.00084;
6; Mismatches 79;
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Wuethrich, C.; Peterhans,
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tumor necrosis factor
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58 PQEEESPNN---
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A; Residues: 1-232 <DRE>
A; Cross-references: UNI
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171-178, 1991
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                                               A; Molecule type: A; Residues: 1-23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL
A; Residues: 1-232 < xUH>
A; Residues: 1-232 < xUH>
A; Cross-references: EMBL:X4859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A; Cross-references: translated the codon GAG for residue 202 as Gly
B; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
Submitted to the EMBL Data Library, January 1991
A; Description: Complete nucleotide sequence of a cDNA encoding porcine tun
A; Reference number: $18965
A; Accession: $18965
A; Reference number: $18965
A; Residues: 1-232 < cCHO>
A; Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
A; Residues: 1-232 < cCHO>
A; Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
B; Pauli, U.; Beutler, B.; Peterhans, E.
Gens B1, 185-191, 1989
A; Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase
A; Reference number: 146659; MUD:90034181; PMID:2478420
A; Reference number: 146659; MUD:90034181; PMID:2478420
A; Residues: 44-232 < cADA>
A; Residues: 44-232 < cADA>
A; Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
A; Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C; Genetics:
A; Introns: 62/3; 78/1; 93/1
C; Superfamily: tumor necrosis factor
C; Keywords: cytockine; cytockine; Gytockine; Gytockine; Gytockine; Cytockine; Gytockine; Gyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                        porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myristylation
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Pred. No. 0.0011;
0; Mismatches 78
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A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein;
C;Keywords: glycoprotein; lipoprotein;
F;19,20/Binding site: myristate (Lys)
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tumor necrosis factor alpha precursor (validated] - human NyAlternate names: cachecting TNRA C;Species: How sapisates factor alpha precursor (validated] - human C;Date: 23-Aug-1905 #text change 09-Jul-2004 C;Accession: A9558; 33453; A3331; A4189; B61478; IS3311; S62610; I54522; A01646; B237 R,Ndwin, G.E.; Naylor; S.L.; Sakeguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D. Nicleic Acids Res. 13, 631-6373, 13965.

R,Ndwin, G.E.; Naylor; S.L.; Sakeguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D. Nicleic Acids Res. 13, 631-6373, 13965.

A,Residues: 1-223 *CHBA A;Residues: 1-233 *CHBA A;Residues: 1-233 *CHBA A;Residues: 1-234 *CHBA A;Resi
                                                                                                              macrophage;
                                                                                                                                                                                                                                                                                                                                --ERGP-QRVAAHITGTRGRSNTLSSPNSKNEKALG
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48;
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|GPQREEQLPNAFQSINPLAQTLRSSSRTPSDKPVAHVVA-
                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                            ore 126; DB 1;
ed. No. 0.0025;
Mismatches 72
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Pred.
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ilarity 22.5%;
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A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g16424
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N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tume A;Reference number: JQ1344; MUID: 92084125; PMID:1748301
A;Accession: JQ1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-Jul-2004
                           -SSRSGH
                                                 SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GCSSYVLLTHTVSRFAVSYEDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Bos primigenius taurus (cattle)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul
C; Accession: I46046; S24641
R; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A; Title: Cloning and characterization of the tandemly arranged bovine
A; Reference number: I46046
A; Reference number: I46046
A; Reference number: I46046
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-204 < CL2>
A; Cross-references: UNIPROT: Q06600; EMBL: Z14137; NID: 9796; PIDN: CAA785
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                                                                                                                                                                                                                            Length 204
                           ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-
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                                                                                                                                     61 TISTVOEKQQNISPLVRERGPQRVAAHITG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor
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C; Superfamily: tumor
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07:41:00

3

Jun

Fri

281

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A; Molecule type: DNA
A; Residues: 1-59,'N',61-205 <NED>
A; Cross-references: UNIPROT:P01374
R; Iris, F.J.M.; Bougueleret, L.; P
                                                                                                          YPDPILLMKSARNSCWSK-
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                                                                                                         K.I.;
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                                                                                                         Nakamura,
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                                                                               ; PID:9339738
                                                                                                                                                                                                                                                                                                                                   necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-a A;Reference number: S62610; MUID:96202967; PMID:8631363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hours
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A; Residues: 1-8 < DNA
A; Residues: 1-8 < DAL>
A; Residues: 1-8 < DNA
A; Residues: 3.1.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A; Title: Myristyl acylation of the tumor necrosis factor alpha precurso: A; Reference number: A59163; MUID: 93018820; PMID: 1402651
A; Reference number: A59163; MUID: 93018820; PMID: 1402651
A; Contents: annotation; identification of myristylated lysines
A; Reference number: A92511; MUID: 85130974; PMID: 3871770
A; Contents: annotation; disulfide bond
C; Comment: Secreted from mitogen-activated macrophages within 4-24 hours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Complex: homotrimer
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimental chilling site: tumor necrosis factor #status experimental chilling site: myristate (Lys) (covalent) #status experimental chilling site: carbohydrate (Ser) (covalent) (partial) #status ex F; 81/Binding site: carbohydrate (Ser) (covalent)
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Comment: Secreted from mitogen-activated macrophages within 4-24 ho
t detriment to normal cells. It can also act synergistically with i
Comment: TNF-alpha and -beta (lymphotoxin) are the products of diff
are produced by different cell types and have different induction
                                                                              GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339
S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.;
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Los:M10988; NID:g339737; PIDN:AAA61198.1; PI
Lyymphokine Res. 7, 175-185, 1988

A; Title: Simultaneous production of natural human tumor necrosis
A; Reference number: A61478; MUID:88301617; PMID:2841543
A; Rocession: B61478
A; Molecule type: protein
A; Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,';
R; Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.;
Eur. J. Biochem. 152, 515-522, 1985
A; Title: Molecular cloning and expression of human tumor necrosis
A; Reference number: I53311; MUID:86030296; PMID:3932069
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-233 < MAR>
A; Cross-referra
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0.0044;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:120441; OMIM:191160
A; Map position: 6p21.3-6p21.3
A; Introns: 62/3; 78/1; 94/1
C; Complex: homotrimer
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Immunogenetics 39, 150-154, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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A; Molecule type: pro
A; Residues: 77-99 <7
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A; Molecule type: mRNA
A; Residues: 35-205 <GOE>
R; Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A; Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hyt
A; Reference number: A91906; MUID:87057135; PMID:3536896
A; Reference number: A91906
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-59, N', 61-205 <KOB>
A; Residues: 1-59, N', 61-205 <KOB>
A; Cross-references: GB:D00102; NID:9219913; PIDN:BAA00064.1; PID:9219914
A; Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue 3
R; Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Aug-1985 #sequence revision 07-Jul-1995 #text change 09-Jul-2004
C; Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01
R; Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; J. Cell. Biochem. 29, 171-181, 1985
A; Title: Structure and chromosomal localization of the human lymphotoxin gene. A; Reference number: A92755; MUID:86086150; PMID:3001109
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augus
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A;Title: Haplotypic polymorphisms of the TNFB gene.
A;Reference number: 154482
A;Reference: GB:M55913; MID:g339742; PIDN:AAB59455.1; PID:g339743
A;Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A;Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A;Experimental source: ancestral haplotype 57.1
A;Note: 59-Asn was also found (ancestral haplotype 8.1)
R;Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Ja:Nature 312, 721-724, 1984
A;Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine valances number: A93350; MUID:85086243; PMID:6334807
A;Reference number: A93350; MUID:85086243; PMID:6334807
A; Molecule type: mRNA
A; Residues: 1-205 <GRA>
A; Residues: 1-205 <GRA>
A; Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A; Cross-references: lymphoblastoid cell line RPMI-1788
A; Experimental source: lymphoblastoid cell line RPMI-1788
R; Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Pacold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A; Title: Tumor necrosis factors: gene structure and biological activities. A; Reference number: A32877; MUID:87217059; PMID:3472740
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A;Molecule type: DNA
A;Residues: 1-12,'R',14-205 <IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
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1 A; TNF beta; tumor necrosis factor beta
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A; Status: preliminary; not compared with conceptual translation
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Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a poter
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                      or-alpha,
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R; Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A; Title: Molecular cloning of the genes coding for tumor necrosis factors: A; Reference number: S03791; MUID: 87298639; PMID: 3040015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLYS
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A;Cross-references: GDB:120442; OMIM:153440
A;Cross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine;
E;1-34/Domain: signal sequence #status predicted <NGS-
F;1-34/Domain: signal sequence #status predicted <NAT>
F;35-205/Product: lymphotoxin #status predicted <NAT>
F;41/Binding site: carbohydrate (Thr) (covalent) #status experimental
                     fact
                                                                                                                                                                                                Vari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 day while having no detrimental effect on normal cells. It can also act C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the ical activities but are produced by different cell types and have dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIN
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C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Ju
C; Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058;
R; Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A; Title: Cloning and expression in Escherichia coli of the gene for r
                                                                                                                                                                                                                                                                                                                                                                                                    human lymphoto
                        necrosis
                                                              A; Accession: A61478
A; Accession: A61478
A; Molecule type: protein
A; Residues: 56-79; 86-95, 'X', 97, 'X', 99; 119-151, 'XX', 154-162, 'X', 154; Noigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A; Title: Natural human tumor necrosis factor beta (lymphotoxin)
A; Reference number: S26951; MUID: 93083656; PMID: 1451807
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                    stion of natural human tumor MUID:88301617; PMID:2841543
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                                                                                                                                                                                                                                                                                                                                                                                                                               PMID:8323280
                                                                                                                                                                                                                                          A; Accession: S26951
A; Molecule type: protein
A; Residues: 35-59,'N',61-205 < VOI >
A; Residues: 35-59,'N',61-205 < VOI >
A; Note: 60-Thr was also found
R; Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; A
Arch. Biochem. Biophys. 304, 144-153, 1993
A; Title: N-linked sugar chain structure of recombinant
A; Title: N-linked sugar chain structure of recombinant
A; Contents: annotation
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No. 0.0046;
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ilarity 23.4%;
Conservative 25
                 A; Title: Simultaneous production A; Reference number: A61478; MUID
1988
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175-185
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A; Residues: 1-235 <SHI>
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A, Molecule type: DNA
A, Residues: 1.235 -681A.
A, Ancier Caricle in Russian with English abstract
R, Somon, D.; Kawahima, E.; Jonganeel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nyittle: Nucleocide sequence of the murine TYP locus, including the TYP-alpha
A, Accession: A27303
A, Accession: A27303
A, Accession: A27303
A, Accession: A27304
A, Residues: 1.235 -681A
A, Residues: 1.230 -681A
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A; Introns: 62/3; 81/1; 97/1
A; Note: the first intron occurs in the 5'-untranslated region
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lympho)
F; 80-235/Product: tumor necrosis factor #status experimental <MAT>
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 148-179/Disulfide bonds: #status predicted
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tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: $22052
R;Sanjanwala, M.; Edwards, A.
R;Sanjanwala, M.; Edwards, A.
Submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Recession: $22052
A;Accession: $22052
A;Accession: $22052
A;Molecule type: DNA
A;Molecule typ
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NAlternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic shorison 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: JH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A;Title: Sequence of the cDNA encoding ovine tumor necrosis fact
A;Reference number: JH0529; MUID:92112044; PMID:1765267
A;Accession: JH0529
A;References: ulveolar macrophage
R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A;Title: Molecular cloning, expression and characterization of A;Reference number: S48118; MUID:92155784; PMID:1786996
A;Accession: S48118
A;Accession: 
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A; Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205
A; Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205
R; Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A; Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffe A; Reference number: S21674; MUID:92329007; PMID:1627266
A; Accession: S21674
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A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146
C;Comment: Tumor necrosis factor is secreted by macrophages in respon
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A; Cross-references: UNIPROT: P16599
R; Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A; Title: Cloning and sequence analysis of the rat tumor
A; Reference number: JN0868; MUID: 94040766; PMID: 8224868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                      tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #to
C;Accession: JU0029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli or
A;Reference number: JU0029
A;Accession: JU0029
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A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
DPILLMKSARNSCWSKDAEYG-
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C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F; 42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 106-138/Disulfide bonds: #status predicted
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                                                                                                                                                     glycoprotein;
                                                 A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-62,64-234 < YOU>
A; Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g14
A; Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g14
A; Note: comparison with the introns of homologous sequences suggest
C; Superfamily: tumor necrosis factor
C; Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein;
C; Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein;
F; 1-77/Domain: propeptide #status predicted <F; 18-234/Product: tumor necrosis factor alpha #status predicted
F; 18-234/Product: tumor necrosis factor alpha #status predicted
F; 20/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 146-178/Disulfide bonds: #status predicted
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C; Species: Capra aegagrus hircus (domestic goat)
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #te
C; Accession: S06192; S41867
R; Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A; Reference number: S06192
A; Accession: S06192
A; Molecule type: mRNA
A; Residues: 1-193 <GOL>
A; Cross-references: UNIPROT: P13296; EMBL: X14828; NID: goat)
                                                                                                                                                                                                                                                                                                           Score 117.5; DB 1;
Pred. No. 0.013;
0; Mismatches 78;
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  S13114; MUID:91067496; PMID:22511
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number: S41867
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A; Reference number: S
A; Accession: S13114
A; Status: preliminary
A; Molecule type: mRNA
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A; Residues: 36-38,'S'
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A; Residues: 1-202 <SEM>
A; Cross-references: UNIPROT: P09225; GB: Y00467; NID: 954830; PIDN: CAA68529.1; PID: 954831
A; Cross-references: UNIPROT: P09225; GB: Y00467; NID: 954830; PIDN: CAA68529.1; PID: 954831
B; Nucleic Acids Res. 14, 7713-7725, 1986
A; Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are A; Reference number: S01342; MUID: 87040736; PMID: 3490653
A; Accession: S01342
A; Molecule type: DNA
A; Residues: 1-11;139-160, 'CG', 163-178 <NED>
A; Cross-references: EMBL: X06217
B; Weil, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A; Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA b; Reference number: S10083; MUID: 89144562; PMID: 3147435
A; Accession: S10083;
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A; Residues: 6-202 <WEI>
A; Residues: 6-202 <WEI>
A; Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
A; Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R; Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A; Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis
A; Reference number: I56004; MUID:87252204; PMID:2885372
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A;Cross-references: GB:M16819; NID:g202088; PIDN:AAA40460.1; PID:C;Comment: The first intron occurs in the 5'-untranslated region. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change C; Accession: B27303; S01342; S10083; IS6004; I48853; IS5980 R; Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedo Nucleic Acids Res. 15, 9083-9084, 1987
A; Title: Nucleotide sequence of the murine TNF locus, including A; Reference number: A93679; MUID:88067722; PMID:3684584
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-25,'P',27-202 < RES>
A; Cross-references: GB: M17015; NID: g198880; PIDN: AAA39450.1;
B; Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A; Title: The murine tumor necrosis factor-beta (lymphotoxin)
A; Reference number: I48853; MUID: 87231097; PMID: 3588316
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A; Title: Cloning and expression of murine lymphotoxin cDNA.
A; Reference number: 155980; MUID:87224127; PMID:2884262
                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: mRNA
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names: lymphotoxin; TNF beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: 148853
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-202 <RE2>
A; Cross-references: EMBL: Y00137; N
                                     --NISAPGOLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            necrosis factor beta
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A; Molecule type: DN
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CD40 ligand and bc
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: $52715
R;Mertens, B.; Gaidulis, L.
Submitted to the EMBL Data Library, March 1995
A;Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligan
A;Reference number: $52715
A;Reference number: $52715
A;Reference number: $52715
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-185 <MER>
A;Cross-references: EMBL:248808; NID:g755701; PIDN:CAA88743.1; PID:g755702
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein
F;33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;97-129/Disulfide bonds: #status predicted
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                                                                                                                                                                                                             80 GPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH 139
                                                                                                                                                                                                                                                                                                        140 EKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 KSARNSC-----WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
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--LWRASTDRAFLRHGFSLSNNSLLIP 99
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                                                                      macrophage
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159 PWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSSVFFGAF 200
A; Map position: 17
A; Introns: 32/3; 66/1
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                              199 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
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Pred. No. 0.021;
9; Mismatches 79;
                                                                                                                                                              81;
                                                                                                                    1;
                                                                                                                Score 114; DB 1
Pred. No. 0.021;
25; Mismatches
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Best Local Similarity 25.0%; Pr
Matches 45; Conservative 29;
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GILKPAAHLVGYPSKQNSL-
                                                                                                                   8.9%;
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Best Local Similarity 23.5
Matches 38; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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- protein search, using sw model OM protein

3, 2005, 06:15:49 June Run. on:

; Search time 40 Seconds
 (without alignments)
 675.923 Million cell updat

es/sec

281

US-10-662-431-2 1478

1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 283416 seqs, 96216763 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

IR 79: *
pir1: *
pir2: *
pir2: * 4 0 6 4

a cinted, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

	Description	ligand - m	_	fas ligand - rat	ligand -	ligand - h	r necrosis	CD40 ligand - mous	sis f	tumor necrosis fac	8 f	8 F	ω	tumor necrosis fac	Д	вiв	8	necrosis	11	necrosis	tumor necrosis fac	ω	tumor necrosis fac	lymphotoxin-beta -	mRNA maturase b14	tumor necrosis fac	amphotropic murine	is	toxin bet	probable membrane
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tumor necrosis fac	protein kinase, pr	A ligase homol	tical pro	tical	netical pro	ain	heat shock transcr	cardiac muscle fac	myosin-light-chain	rine/threonine	activin receptor-1	hypothetical prote	chetical	O	alpha-N-arabinofur
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233	448	345	365	455	B	1465	833	m	1176		0	1284		313	328
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	7.5	92	95	92	94.5	94	92.5	7	σ	90.5	0	0	90	89.5	8
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ALIGNMENTS

d - mouse hus muscu 6-Jan-1995 on: A53062 hi, T.; Tar 969-976, 19 Generalize Ce number: on: A53062 preliminan e type: mRP s: 1-279 <7 cal Similan cal Similan 51; Cor 83 QLRQLV 143 NEKALC 143 NEKALC 155 SIPL 203 DKQMV(:: : 202 NQPLNF 261 TNEHL) 260 SQLSL) 260 SQLSL)	RESULT 1 A53062 Fas ligand - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004	laka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nage 394	A53062; MUID:94185175; PMID:7511063 ry NA RAK> UNIPROT:P41047; GB:U06948; NID:9473564; PIDN:AAA17800.1; PID:9473565	l 12.8%; Score 189.5; DB 2; Length 279; Similarity 25.8%; Pred. No. 1.7e-08; 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;	RKMILRTSEETISTVOEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSK 142	: : : : : : : : : : : : :	NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSOTYFRFOEEIKENTKN 202		DKOMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260	:: : : : : :	TNEHLIDMDHEASFFGAF 278	SQLSLINFEESKTFFGLY 277
	d - mouse : Mus musculus 6-Jan-1995 #se	hi, T.; Tanaka 969-976, 1994 Generalized ly	A; Reference number: A53062; MUID A; Accession: A53062 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-279 <tak> A; Cross-references: UNIPROT: P410</tak>	Query Match Best Local Similarity Matches 51; Conser								

RESULT 2
138707
Fas ligand - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: 138707; JC2340; S57565; 138554
C; Accession: 138707; JC2340; S57565; 138554
R; Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A; Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A; Reference number: 138707; MUID: 95127560; PMID: 7826947
A; Reference number: 138707
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-281 < RES>
A; Cross-references: UNIPROT: P48023; EMBL: U11821; NID: 9595430; PIDN: AAC50124.1; PID: 959542

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                                      virue
                                                                                                                         PIDN: BAA0732
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A, Cross-references: EMBL:X89102, NID:g887455; PID:g887456
R; Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B. J. Exp. Med. 181, 71-77, 1995
A; Title: Fas ligand mediates activation-induced cell death in human A; Reference number: 138554; MUID:95105731; PMID:7528780
A; Accession: 138554
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Cross-references: EMBL: U08137; NID: 9624627; PIDN: AAC50071.1;
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R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; K
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis
A;Reference number: JC2340; MJID:95071350; PMID:7980502
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Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand,
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
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                                                                                    A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <TWW>
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Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <
F;76,184,250,260/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: glycoprotein; transmembrane protein
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S57565
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                                                                                                                                      R;Schatzlein, C.E.
submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-281 <SC
                                                                                                                                                                                       A;Accession: S57565
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                     A; Accession: JC2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A49266
                                                                                                                                                                          A; Reference number
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CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP prote
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
C;Accession: S28017; JH0793; $26694; S28852; I53476; S25684; S30593
C;Accession: S28017; JH0793; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C; Accession: S53090
R; Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A; Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A; Reference number: S53090
A; Cccssion: S53090
A;
                                                                                                                                                                                                                                                                                                                                                                                                              VOGGPSLGQTCVLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QW--APKGYYTLSNNLVTLENGKQLAVKR
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                                                                                                                                                                                                                                                     SCHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP
                                                                                                                                                                                                                                                                                                              -SCNSQPLSHKVYMRNFKYÞ
                                                                                                                                                                                                                                                                                                                                                                             DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
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        2;
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Pred. No. 2.3e-06;
; Mismatches 114
                                                                                                                                                                 LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
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QQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFG
                             ed. No. 1.8e-07
Mismatches 64
          DB
                                                                                                                                                                                                                                                                                 Score 177.5;
Pred. No. 1.8
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larity 27.5%;
Conservative
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larity 25.9%;
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Best Local Similarity
Matches 72; Conser
Query Match
Best Local Similarity
Matches 50; Conser
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Hayashi,

J.;

Kiyota,

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Kajihara,

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Best Local
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2 in having
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B.M.;
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                                                                      NID:938483; PIDN:CAA78737
Clifford, K.N.; Macduff,
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--ILLRAANTHSSAKPC-
                                                                                                                                                                                                                                                                                                                                                                                                              270
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T.; Elson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:91
                                                  A; Residues: 1-261 <HOL>
A; Residues: 1-261 <HOL>
A; Cross-references: UNIPROT: P29965; EMBL: Z15017; NID: g38483; PIDN: CAA; Cross-references: UNIPROT: P29965; EMBL: Z15017; NID: g38483; PIDN: CAA R; Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macd J. Exp. Med. 176, 1543-1550, 1992
A; Title: Recombinant human CD40 ligand stimulates B cell proliferatio A; Title: Recombinant human CD40 ligand stimulates B cell proliferatio A; Reference number: JH0793; MUID: 93094757; PMID: 1281209
                                                                                                                                                                                                A;Residues: 1-261 <SPR>
A;Residues: 1-261 <SPR>
A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g3841
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule Jr.:
Residues: 1-261 <GAU>
Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A25454; A25451; JS0727
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                                                                                                                                                                                                                                                                                                                                                                                                 es: EMBL:X68550; NID:g37269; PIDN:CAA48554.1, Aubry, J.P.; Mazzel, G.; Life, P.; Jomotte, 259-266, 1993
                                                                                                                                                                                                                                                                                                cells
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                                                                                                                                                                                                                                                                                                                                        R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kro
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T
A;Reference number: S26694; MUID:93076854; PMID:1280226
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 PMID:1385114
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C; Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 147.5; DB 2; larity 23.7%; Pred. No. 5.7e-05; Conservative 51; Mismatches 99;
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 S28017; MUID:93049181;
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nes 66; Conser
                                                                                                                                                                                    mRNA
                                   A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
A; Accession: S28852
A; Molecule type: mRA
                                                                                                                                                                A; Accession: JH0793
A; Molecule type: mR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDB: CD4 0LG;
                                                                                                                                                                                                                                                                                                                                   A;Accession: S26694
A;Status: prelimina
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor
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A/Cross-references: UNIPROT: P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1;

R/Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wa DNA 5, 157-165, 1986

A/Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor A/Reference number: A25451; MUID:86219712; PMID:3519138

A/Accession: A25451

A/Accession: USO727

A/Acces
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                                                                              CDNA
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                                                                              coli
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R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajiha
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Rocession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
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Nature 357, 80-82, 1992
A; Title: Molecular and biological characterization of a A; Reference number: S21738; MUID: 92244364; PMID:1374165
A; Accession: S21738
A; Molecule type: mRNA
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larity 22.4%; Pred. No. 0.00017;
Conservative 41; Mismatches 98
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PIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFG
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C;Date: 31-Dec-1993 #sequence_revision
C;Accession: S21738
R;Armitage, R.J.; Fanslow, W.C.; Strock
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--VIGPOKEEFPAGPL
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     46448.1;
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C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <MAT>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>
                                                                                                                                                                                        17 VLIVIFIVLL - OSLCVAVTYVYFINELKOMODKYSKSGIACFLKEDDSYWDPND
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                                                                                                                                                                                                                                                                                                                                         SNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIY
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A;Cross-references: UNIPROT:P27548; EMBL:X65453; NID:g50351; PIDN:C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TMM>
F;47-260/Domain: extracellular #status predicted <EXT>
F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Accession: S17289
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-204 < KUH>
A; Cross-references: UNIPROT: P26445; EMBL: X54859; NID: 92132; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_c
C;Accession: S17289
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes:
A;Reference number: S17289; MUID:91340150; PMID:1874444
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                                                                                                                                                      104;
                                                                                                                Score 141; DB 2;
Pred. No. 0.0002;
); Mismatches 104
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|larity 23.5%;
|Conservative 5
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Best Local Similarity
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Best Local S
Matches 59
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A; Kesldues: 1-232 < CHO>
A; Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R; Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A; Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chains, Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chains, Reference number: 146659; MUID:90034181; PMID:2478420
A; Reference number: 146659; MUID:90034181; PMID:2478420
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 44-232 < PAU>
A; Residues: 44-232 < PAU>
A; Residues: 64-232 < PAU>
A; Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C; Genetics:
A; Introns: 62/3; 78/1; 93/1
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrop F; 1-77/Domain: propeptide #stetus predicted < PAT>
F; 19, 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 81/Binding site: myristate (Ser) (covalent) #status predicted
F; 144-176/Disulfide bonds: #status rrandicted
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Superfamily: tumor necrosis factor

; Superfamily: tumor necrosin; glycoprotein; lipoprotein; lymphokine;

;1-77/Domain: propeptide #status predicted <PRO>

;78-232/Product: tumor necrosis factor alpha #status predicted

;19,20/Binding site: myristate (Lys) (covalent) #status predicted

;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

;144-176/Disulfide bonds: #status predicted
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A; Cross-references: UNIPROT: P23563; EMBL: X54001; NID: 92135; PIDN R; Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U. Gene 102, 171-178, 1991
A; Title: The porcine tumor necrosis factor-encoding genes: seque A; Reference number: S17289; MUID: 91340150; PMID: 1874444
A; Reference number: S17289; MUID: 91340150; PMID: 1874444
A; Residues: 1-232 < KUH>
A; Residues: 1-232 < KUH>
A; Residues: 1-232 < KUH>
A; Residues: 1-32 < KUH>
A; Residues: 1-33 < KUH>
A; Reference con a con GAG for residue 202 as R; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
Submitted to the EMBL Data Library, January 1991
A; Description: Complete nucleotide sequence of a cDNA encoding p A; Accession: S18965
A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
A; Molecule type: mRNA
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A; Molecule type: mRNA
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                                                                                                  #text
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor
A;Reference number: S12606; MUID: 91016861; PMID: 2216741
A;Accession: S12606
A;Molecule type: DNA
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F;19,20/Binding site: myristate F;82/Binding site: carbohydrate F;146-178/Disulfide bonds: #stat
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Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF
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E endotoxemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Ju
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
                                                                                                                         <u>-</u>5
                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P33620; EMBL: X62141; NID: 938159; PIDN: CAA
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equi
A;Title: Cloning and characterization of gene TNF alpha encoding equi
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA3
C;Comment: This protein is an important proximal mediator of endotoxe
                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                              A; Introns: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane
F; 19,20/Binding site: myristate (Lys) (covalent) #status predicted
F; 81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85;
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  228
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                                                                                                                         change
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  EGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG
                                                                                                                         #text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                   C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 131.5; DB Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                       baboon
                                                                                      necrosis factor alpha precursor
sies: Papio sp. (baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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nilarity 19.2%;
Conservative 49
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                                                                                                                                                                                                                                                                                <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVAHVVA-
                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                              type: DNA: 1-233 <SP
                                                                                                                                                                                                                             A; Accession: S22052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GCPSTHVLLTHTISRLAVSYPSKVNLLSAIKSPCHTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVR
                                                                                                                                                                                                                                                             EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP
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                                                                                                                                                                                                                   -CLLHFGVIGPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: CAA78511
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C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 145-177/Disulfide bonds: #status predicted
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predicted
predicted
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor alpha precursor - bovine
C; Species: Bos primigenius taurus (cattle)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_chang
C; Date: 10. Sep-1999 #text_chang
C; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans,
C; Considered Characterization of the tandemly arranged
A; Reference number: 146046; MUID:94083525; PMID:8260599
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-233 < CL2>
A; Residues: 1-233 < CL2>
A; Coss-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PID
C; Genetics:
A; Gene: TNFA
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   #status
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Pred. No. 0.0013;
3; Mismatches 95;
                                                                                                                               89;
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ed. No. 0.0012;
Mismatches 8
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  (covalent)
(covalent)
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                                            #status predicted
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Pred.
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  (Lys)
(Ser)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: I46046; S24641
R; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A; Title: Cloning and characterization of the tandemly arranged bovine lympha; Title: Cloning and characterization of the tandemly arranged bovine lympha; R; Reference number: I46046; MUID: 94083525; PMID: 8260599
A; Accession: I46046
A; Accession: I46046
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-204 < CL2>
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A;Residues: 1-235 <RES>
A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA4
                                                                                                                                                                 -Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIPROT: Q06600; EMBL: Z14137; NID: 9796; PIDN: CAA78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TRGRSNTLSSPNSKNEKA
  276
                                   229
                                                                                                                                                                                                                                          gene
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                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status predicted #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204;
--WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
                  |: :|: :|: :|||||:|:|: ||: : :|: :| :|: :|| TPEWA-EAKPWYEPIYQGGVFQLEKGDRLSAEINLPDYLDYAESGQVYFG
                                                                                                                                                                #text_change
                                                                                                                                                                                                                                      (TNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                        tumor necrosis factor alpha precursor - white-footed mouse C; Species: Peromyscus leucopus (white-footed mouse) C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_chacession: 154490
R; Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A; Title: Sequence of the tumor necrosis factor/cachectin (1888) R; Reference number: 154490; MUID: 92218012; PMID: 1348497
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; myristylation
(covalent) #stal
(covalent) #stal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 129.5; DB 2; 24.5%; Pred. No. 0.0016; ive 39; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127.5; DB 1;
Pred. No. 0.002;
9; Mismatches 78;
                                                                                                                                                                                                                                                                       A; Accession: I54490
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISTVQEKQQNISPLVRERGPQRVAAHITG--
                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 62/3; 81/1; 97/1
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein;
F;19,20/Binding site: myristate (Lys)
F;84/Binding site: carbohydrate (Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.6%;
llarity 24.9%;
Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Introns: 32/3;
C;Superfamily: tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 45
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Best Local S
Matches 47
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                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: PlTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                        RESULT
                                  <del>Q</del>
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tumor necronis factor alpha precursor [validated] - human

Cubecies: How ospision can cachectling TRFA

Cipaceis: How ospision can cachectling the cache cachectling the cach
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                                                                                                                                                                                                                      KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD
                                                                                                                                                                                                                                                            -SLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPLYLAHEVQ
                                                                          NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRPQEEIKENTKNDKQMVQYIY
-DRAFLR-
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7

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A;Cross-references: GB:MX6331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
B;Takakura-Yamamoto, R; Yamamoto, S; Fukuda, S; Kurimoto, M.
Bur. J. Blochem. 235, 431-437, 1996
B;Takakura-Yamamoto, R; Yamamoto, S; Fukuda, S; Kurimoto, M.
Bur. J. Blochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Roference number: 562610; MUD:96202967; PMID:8631363
A;Rofession: 562610
A;Rofession: 562610
A;Rofession: 562610
A;Rofession: 562610; MUD:94102809; PMID:7903959
A;Rofession: 154522
A;Rofession: 154523
A;Rofession: 15452
A;Rofession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-24 hours after inductior with interferon gamma to of different genes closely fuction kinetics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NPQAEGQL--QWLNRRANALLANGVELRDNQLVVPSEGL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR
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A; Map position: 6p21.3-6p21.3
A; Introns: 62/3; 78/1; 94/1
C; Complex: homotrimer
C; Complex: homotrimer
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein
E;1-76/Domain: propeptide #status predicted <PRO>
F;1-76/Domain: propeptide #status factor #status experimental
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status ex
F;145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: Secreted from mitogen-activated macrophages within 4-24 ho out detriment to normal cells. It can also act synergistically with i C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of diff ut are produced by different cell types and have different induction A;Gene: GDB:TNF; TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
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Best Local Similarity 17.8%; Pred. No. 0.0036;
Matches 51; Conservative 52; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3, 2005, 06:25:41
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OM protein - protein search, using sw model

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281

US-10-662-431-2 1478 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

1612378 seqs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_gprot:*
2: uniprot_trembl:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ch DB ID Descr	81 1 TN10 HUMAN	87 2 Q8K3 <u>G</u> 0 rattu	91 1 TN10 MOUSE P50592 mus mus	04 2 Q7T1F2 Q7t1f2	299 2 Q6DHG9 prachydanio	17 2 Q7ZYX9 Q7ZYX9	87 2 Q90WT9 Q90wt9	14 2 Q9DDZ5 Drac	3 2 Q6JSD9 Q6jsd9	1 TN11_RAT Q9ese2 r tu	1 TN11 MOUSE	17 1 TN11_HUMAN	79 1 TNF6 MOUSE	80 1 TNF6_CERTO Q9bdn1 cercoc	81 1 TNF6 HUMAN	80 1 TNF6_MACFA P63308 macaca	80 1 TNF6 MACMU	80 1 TNF6 MACNE	Q7TMV9 mus	72 1 TNF5_CHICK	82 1 TNF6_PIG Q9bea8 Bus	52 2 Q8K3 <u>Y</u> 8 mus mus	80 2 Q861W5	8 1 TNF6_RAT	69 2 Q9WV <u>9</u> 0	52 2 Q80YZ0 C	52 2 Q8K3Y7 rattu	51 2 Q8NFE9	61 1 TNES BOVIN DS1749 DS	D SOT CELTES WILDER STILL I IS
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TN14 HUMAN	Q8MJ <u>1</u> 9	Q7T2Q3	TN14 MOUSE	TNF5 CALJA	TNF5 AOTTR	TNF5 FELCA	Q6U8 <u>1</u> 7	TNF5 CERTO	TNF5 MACMU	TNF5 CANFA	TNF5 HUMAN	070332	TNF5_PIG
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ALIGNMENTS

SULT 1: 10 HUMAN STANDARD . 201	P50591;	01-OCT-1996 (Rel. 34, Creat 01-OCT-1996 (Rel. 34, Last	25-OCT-2004 (Rel. 45, Last annotation update)	lumor necrosis ractor apoptosis inducing lic	Name=TNFSF10; Synonyms=APO2L, TRAIL;	Homo sapiens (Human Eukarvota: Metazoa:	Mammalia; Eutheria; Primates; Catarrhini; Hominidae	NCBI_TaxID=9606;	SEQUENCE FROM	MEDLINE=96111955;	A Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang CP., A Nicholl J.K. Sutherland G.R. Davis-Smith T. Ranch C., Smith C.A.	Goodwin R.G.;	"Identificati	that induces	[2]		TISSUE=Placenta;		Ashkenazi A.:	"Induction of	necrosis factor cytokine family." T Riol Chem 271.12687-12690(19	[3]		TISSUE	Straus	Klausn	Hopkin	Diatch	Staple	Browner Raha S	Bosak	Richards	Fahev	Whiting	ВТакев	Rodriguez A.C	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;	Generation	
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X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

X-Choi Y.H., Sung B.J., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin H.C.,

X-Choi Y.H., Sung B.J., Shin H.C.,

X-Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin H.C.,

X-Cha S.-S., Shin H.C.,

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                                                                                                                                                                                                                               PubMed=10542098; DOI=10.1038/14935;
Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
Jones E.Y., Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals mechanisms conferrin
specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
                                  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80;
Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.
Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in complex with death receptor 5.";
Mol. Cell 4:563-571(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
GO; GO:0007165; P:positive regulation of I-kappaB kinase/NF-k.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008063636; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein (Potential)
TISSUE SPECIFICITY: Widespread; most predominant in spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor
                    99:16899-16903 (2002)
                                                                                                                                                                                                                (2.2 ANGSTROMS) OF 119-281
0.1038/14935;
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SIMILARITY: Belongs to the tumor necrosis
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EMBL; U57059; AAB01233.1; -.
EMBL; BC032722; AAH32722.1; -.
PDB; 1D0G; X-ray; A/B/D=114-281.
PDB; 1D2Q; X-ray; A=114-281.
PDB; 1D4V; X-ray; B=119-281.
PDB; 1DG6; X-ray; A=91-281.
PDB; 1DG6; X-ray; D/E/F/J/K/L=114-281.
PDB; HGNC:11925; TNFSF10.
H-InvDB; HIX0003863; -.
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A.
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TO-OCT-2002 (TrEMBLrel. 22, Last sequence update)
TO-OCT-2002 (TrEMBLrel. 26, Last annotation update)
TO-MAR-2004 (TrEMBLrel. 26, Last annotation update)
TNF-related apoptosis inducing ligand.
TNF-related apoptosis inducing ligand.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
NCBI_TaxID=101
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Signal-anchor for type II
protein (Potential).
Extracellular (Potential).
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Pred. No. 4.4e-113;
0; Mismatches 0;
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MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;

Miley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,

Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

Goodwin R.G.;

"Identification and characterization of a new member of the TNF family that induces apoptosis.";

"Identification and characterization of a new member of the TNF family That induces apoptosis.";

I mmunity 3:673-682(1995).

"Immunity 3:673-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family
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                                                                                                                                                                                                                                                                                                                                  WDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG
                                                                                                                                                                                                                                                                    EDDSY
                                                                                                                                                                                                                                                                                                                                                                                (GFYYI
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uB
                                                                                                                                                                                                                                                     GPSLGQ----TCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL
                                                                                                                                                                                                                                                                                                                                                                                HITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE
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                                                                                                                                                                                                                                                                                                                                                                                                129 HITGITRRSNLALIPISKDGKTLGQKIETWESSRRGHSFLNHVHLRNGELVIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TNF-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential)
TISSUE SPECIFICITY: Widespread.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEA
                                                                                                                                                                                        287;
 factor receptor binding; ; IEA.
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 10
apoptosis inducing ligand) (TRAIL protein).
Name=Tnfsf10; Synonyms=Trail;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 65.2%; Score 963; DB 2; 1 Similarity 67.7%; Pred. No. 8.5e-71; 189; Conservative 29; Mismatches 51;
                                                                                                                                                         CA4F5B5D7C833FEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $
GO; GO:0005164; F:tumor necrosis fa
GO; GO:0006955; P:immune response;
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
                                                                                    Prodom; PD002012; TNF Bubf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; UNKNOWN-PROSITE; PS50049; TNF 2; 1.
SEQUENCE 287 AA; 32979 MW; CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                           J362
TNF; 1
TNF BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPISKDGKTLGQKIESWESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SEQUENCE FROM N.A.
TISSUE=Spleen;
Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
Sayed A.A., Horiuchi and Characterization of Chicken Tumor Necrosis
"Molecular Cloning and Characterization of Chicken Tumor Necrosis
Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
Inducing Ligand (TRAIL).";
J. Vet. Med. Sci. 66:643-650(2004).
                                                                                                                                                                                                                                                                                                                                                                                               -anchor; Transmembrane.

Cytoplasmic (Potential).

Signal-anchor for type II membrane
protein (Potential).

Extracellular (Potential).

N-linked (GlcNAc. ..) (Potential).

W; 3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane
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Last annotation update)
ed apoptosis inducing li
                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane
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Pred. No. 4.4e-68
; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290
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                                                                                                                           EMBL; U37522; AAC52345.1; -.
HSSP; P50591; 1D2Q.
MGD; MGI:107414; Tnfsf10.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Apoptosis; Cytokine; Signal-ancho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
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Eukaryota, Metazoa, Chordata, (
Archosauria, Aves, Neognathae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 N
33477 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Cr
01-OCT-2003 (TrEMBLrel. 25, La
01-MAR-2004 (TrEMBLrel. 26, La
Tumor necrosis factor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.6%;
Matches 177; Conservative
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us-10-662

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Jones S.J., "Generation
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Best Local S
Matches 121
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                                                     SEQUENCE
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Q7ZYX9
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E.,
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                                                                                                                                                                                                                                                                                          SYWDP
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S.J.,
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S.₩.,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifor
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                   GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                                                                                                                                                                                                                                               ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                                        --IKENTKNDKOMVQYIYKYTSYPDPILLMKSA
                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                  SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
        GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
                                                                                                                                                 304;
                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                      Indels
                                                                                                                             DFC128B517747C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                Score 809.5; DB 2;
Pred. No. 3.6e-58;
5; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                            34658 MW;
                                                                                  subf; 1
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                                                                                                                                               54.8%;
                                                                                           SM00207; TNF; 1.
                                                                                                                                                                      Conservative
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                                                                                   TNF
                                                                                                                             304 AA;
                                                                                                                                                            Local Similarity
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                                                                                 PD002012;
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NCBI_TaxID=7955;
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25-OCT-2004
25-OCT-2004
                                                                                                                                                                     160;
                                                                                            SMART; SM
PROSITE;
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                                                                                                                                                 Query Match
Best Local
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                                                                                                                             SEQUENCE
                                                                                                                 PROSITE;
                                                                                  ProDom;
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                  full-length human
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; Cypriniforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                        IEA
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                                                                                                                                                                                                        receptor binding
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Craniata; Vertebrata; El
Teleostei; Ostariophysi;
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                   15,000
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Last sequence update)
Last annotation update)
                                     sequences.";
id. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                      TISSUE=Whole;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ dat
EMBL; BC076005; AAH76005.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
                                                                                                                                                                                                                                                                                                                                                                                                                             39.1%; Score 577.5; DB 2; larity 42.2%; Pred. No. 3.9e-39; Conservative 57; Mismatches 82;
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SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 299 AA; 33526 MW;
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-JUN-2003 (TrEMBLrel
-OCT-2003 (TrEMBLrel
Marra M.A.
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TNF; TNF
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                                    and mouse cDNA sec
Proc. Natl. Acad.
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FROM N.A
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InterPro; IPR0
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SEQUENCE
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding;
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF-related apoptosis inducing ligand-like protein.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                         22.6%; Score 334.5; DB 2; llarity 29.2%; Pred. No. 3.7e-19; Conservative 55; Mismatches 113;
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35465 MW;
                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body
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P50591; 1D2Q.
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Submitted (JAN
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18 LIVIFTVLLQ--SLCVAVTYVYFT-----NELKQM--QDKYSKSGIACFLKEDDSYWD
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Bobe J., Goetz F.W.;

"Molecular cloning and expression of a TNF receptor and tw ligands in the fish ovary.";

Comp. Blochem. Physiol. B, Comp. Biochem. 129:475-481(2001)

EMBL; AF250041; AAG47640.1; -.

HSSP; P50591; 1D2Q.

ZFIN; ZDB-GENE-010801-1; tnfsf101.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                               20.8%; Score 307.5; DB 2; 32.3%; Pred. No. 5.3e-17; ive 46; Mismatches 110;
                             Johnson A.L.;
2001) to the EMBL/GenBank/DDBJ
Bridgham J.T., Johnson ...

Submitted (OCT-2001) to the EMBL/Ge...

EMBL; AY057941; AAL23702.1; -.

HSSP; P50591; 1D2Q.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

R Pfam; PF00229; TNF; 1.

R PRINTS; PR01234; TNECROSISFCT.

ProDom; PD002012; TNF subf; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS50049; TNF 2; 1.

PROSITE; PS50049; TNF 2; 1.
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IPR006052; TNF family.
IPR008983; TNF like.
IPR003636; TNF subf.
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24093 MW;
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SMART; SM00207; TNF; 1
PROSITE:
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PROSITE; PS50049; TNF
SEQUENCE 214 AA; 2
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01-OCT-2003 (TrEMBLr
TRAIL-like protein.
Name=tnfsf101;
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Best Local Similarity
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor act of nuclear factor kappa B ligand) (RANKL) (TNF-related activation induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Oste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Tibial bone;
MEDLINE=20540945; PubMed=11092398;
Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki
                                                                                                                                                                                                                                                                                                                                            Euteleostomi
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                               --LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHI
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214;
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                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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  Length
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|DAEYALHSVYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAF
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Mannila H., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8F0C7936DASAA6E6 CRC64;
                                                                                                                                                                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; L
Lu. No. 1.7e-16;
Mismatches
            7;
 DB 2;
Score 305.5; DB Pred. No. 5.3e-177; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; AY312579; AAR16184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
                                                                                                                                                                                                                                                                                                                                                                                                                    elin J., West
Laitinen T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synonyms=Opgl, Rankl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred
                                                                                                                                                                                                                                                                                                                                                                                                                    Vendelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                     37;
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ODE)
20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                  Polvi A., Ruosaari S., Vende
Reinikainen A., Hollmen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7638 MW;
                                                QRVAAHITGTRGRSNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.7%
                                                                                                                                                                                                                                                                                     04 (TrEMBLrel. 2
tumor necrosis
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation factor)
Name=Tnfsf11; Synonyms=C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung carcinoma;
                                                                                                                                                                                                                                                                                                                                 (Human)
         l Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 52; Conser
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazo
Mammalia; Eutheri
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ESE2; Q91Z19;
                                                                                                                                                                                                                                                                                                                      Name=TNFSF10;
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                         05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                 5-JUL-2004
                                                                                                                                                                                                                                                                                                         (Fragment)
                                                                                                                                                                                                                                                                                             Chemokine
Query Match
Best Local S
Matches 62
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RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
Int. J. Dev. Biol. 45:853-859(2001).

-!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
TNFRSF11A/RANK. Osteoclast differentiation and activation factor.

Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

-!- SUBGUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions on ig as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                         similarity).
TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                         is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LKED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     member 11, soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
Cleavage (By similarity).
N-linked (GlcNAc. . ) (Potential).
I -> M (in Ref. 2).
                                                                                                              C., Mason-Savas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                rat
                                                                                                                                         Marks S.C. Jr.; "Evidence that the rat osteopetrotic mutation toothless (tl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318
               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            member 11, membrane form.
Tumor necrosis factor ligand
member 11, soluble form.
Cytoplasmic (Potential).
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               of
            "Cloning, sequence and functional characterization homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186 (2000).
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NO. 1.2e-13;
                                                                                                             MacKay
                                                                                                             van Wesenbeeck L., MacKay
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Pred.
                                                                                 STRAIN=Fischer 344;
MEDLINE=21662371; PubMed=11804028;
Odgren P.R., Kim N., van Wesenbeec
Safadi F.F., Popoff S.N., Lengner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF187319; AAG17031.1; -.
EMBL; AF425669; AAL23963.1; -.
HSSP; 035235; 1JTZ.
RGD; 620784; Tnfsf11.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_like.
Pfam; PF00229; TNF; 1.
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                                                                    266-318 FROM N.A.
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ilarity 27.3%;
Conservative 55
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CONFLICT
SEQUENCE
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-DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                   --GPO
                                                                     SSRSGH
                                                                                                        --SSWYHDR-GW
                                                                                                                                                                                                                                 255 NLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISVQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                          SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPI
                                                                                                                                                                              (I PSSH
                                                                                                                                                                                                                 FGAFLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X; Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.Y.,
                                                                                                                                                                                                                                                                                                                           MOUSE
TIN11 MOUSE STANDARD; PRT; 316 AA.
O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activation-of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteocidiferentiation factor) (ODF) (Osteoclastogenesis-inhibitory factori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Hybridoma;
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necrosis factor receptor in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A homologue of the TNF receptor and its ligand enhance T-cell and dendritic-cell function.";
Nature 390:175-179(1997).
                                  -GAVORELOHIV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FINC.
TISSUE=Bone marrow stroma;
MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
Yasuda H., Shima S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymic lymphoma;
MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosma
                                                                                                      RFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGSHKVSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi Y.; "TRANCE is a novel ligand of the tumor that activates c-Jun N-terminal kinase Taiol. Chem. 272:25190-25194 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Infsf11; Synonyms=OPGL, RANKL,
                                ODSTLESEDTEALPDSCRRMKQAFQ-
                                                                    --RGRS-
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Mammalia; Eutheria; Rodentia;
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                                                                     R---VAAHITGT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus
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Galibert
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MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
A Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
T. S.2-A resolution.";
J. Biol. Chem. 277:6631-6636(2002).
C -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
C Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
-!- SUBUNIT: Homorrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=3;
IsoId=035235-3; Sequence=VSP_006448;
TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
but not in nonlymphoid tissues and is abundantly expressed in T
cells but not in B cells. A high level expression is also seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                form
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determinants
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MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
"Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a TNF family member involved in osteoclastogenesis and dendritic cell survival."
J. Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                       osteoclast
                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=129;

MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-
Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.

Ueda M., Higashio K.;

"Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the trabecular bone and lung.

PTM: N-glycosylated.

PTM: The soluble form of isoform 1 derives from the membrane by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

DISEASE: Deficiency in Thfsf11 results in failure to form lob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homotrimer.
SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoforms 1 and 2); Cytoplasmic (isoform 3).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of n factor-kappas ligand and their differential expression in bone
                                                   and
           Suda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Teitelbaum S.L., Fremont 3/RANKL cytokine reveals c
Morinaga T., Higashio K., Udagawa N., Takahashi N., S
"Osteoclast differentiation factor is a ligand for
osteoprotegerin/osteoclastogenesis-inhibitory factor
to TRANCE/RANKL.";
Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316 MEDLINE=21464816; PubMed=11581298; Lam J., Nelson C.A., Robs F.P., Teitelbaum S.L., "Crystal structure of the TRANCE/RANKL cytokine of receptor-ligand specificity."; J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sold=035235-2; Sequence=VSP_006449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 142:1419-1426(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing;
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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odysplasia,
rease in
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     leath
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EMBL; AF0134048; AAB86812.1; -.

EMBL; AF01340426; BAA25425.1; -.

EMBL; AB0022039; BAA36970.1; -.

EMBL; AB022037; BAA36970.1; -.

EMBL; AB022037; BAA36970.1; JOINED.

EMBL; AB022037; BAA36970.1; JOINED.

EMBL; AB032771; BAA97257.1; -.

EMBL; AB032772; BAA97259.1; -.

EMBL; AB032772; BAA97259.1; -.

EMBL; AB032772; BAA97259.1; -.

EMBL; AB032772; BAA97259.1; -.

R PDB; 11QA; X-ray; X/Y/Z-146-316.

R PDB; 11QA; X-ray; X/Y/Z-146-316.

R PDB; ITZ; X-ray; X/Y/Z-146-316.

R QC; GC: 00045804; F: protein binding; IPI.

GC; GC: 00045813; P: protein binding; IPP.

GC; GC: 0004587; P: proganogenesis; IMP.

GC; GC: 00045670; P: regulation of osteoclast differentiation; IDA.

R GC; GC: 00045670; P: regulation of osteoclast differentiation; IDA.

InterPro; IPR006052; TNF family.

R InterPro; IPR008983; TNF_like.

InterPro; IPR008983; TNF_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis factor ligand superfam member 11, membrane form.

Tumor necrosis factor ligand superfam member 11, soluble form.

Cytoplasmic (Potential).

Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00207; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
3D-structure; Alternative splicing; Cytokine; Differentiation; 3D-structure; Alternative Splicing; Cytokine; Signal-anchor
alveolar mammary structures during pregnancy, resulting in dof newborns. Trance-deficient mice show severe osteopetrosis no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, inclust the limbs, skull, and vertebrae and have marked chondrodysplawith thick, irregular growth plates and a relative increase hypertrophic chondrocytes.

SIMILARITY: Belongs to the tumor necrosis factor family.
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N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
Missing (in isoform 3).
/FTId=VSP 006448.
SSEEMGSGPGVPHEGPLHPAPSAPAPPPPA ->
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Missing
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Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF subf; 1.
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N11_HUMAN STANDARD;
C 014788; 014723; 096017; 09P2Q3;
C 014788; 014723; 096017; 09P2Q3;
T 16-OCT-2001 (Rel. 40, Last sequence update)
)T 16-OCT-2001 (Rel. 44, Last annotation update)
)T 05-JUL-2004 (Rel. 44, Last annotation update)
)T 05-JUL-2004 (Rel. 44, Last annotation update)
)E Tumor necrosis factor ligand superfamily member 11 (Receptor activation-
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).
GH differentiation factor) (ODF).
GH differentiation factor) (ODF).
GH differentiation factor) (ODF).
Homo sapiens (Human).
Homo sapiens (Human).
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MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
Boyle W.J.;
"Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation.";
Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                   Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell Nature 390:175-179(1997).
                                                                     51;
                                  316;
                                                                                                                                                                                WDP -- NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

TISSUE=Bone marrow, and Peripheral blood;

MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;

Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman
Galibert L.;
                                                                                                        10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF
                                  Length
                                                                      Indels
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                                   1;
                                                                    113;
                                Score 258.5; DB 1
Pred. No. 6.3e-13;
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Ikeda T., Kuroyama H., Hirokawa K.;
"Determination of human RANKL isoforms.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
                                                                     Mismatches
                                                                                                                                                                                                   ODSTLESEDTLPDSCRRMKQAFQGAVQK--
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                                                                      54;
                                17.5%;
larity 26.4%;
Conservative 54
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78; Conserv
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TISSUE=Thymocytes;
                                 Query Match
Best Local S
Matches 78
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                                                                      family
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                                                                                                                                                                                                                                                           Blochem. Biophys. Res. Commun. 269:532-536(2000).

-!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

-!- SUBGUNIT: Homotrimer (By similarity).

-!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3) Secreted (isoform 2). A soluble form of isoform 1 arises by proteolytic processing (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=3;
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IsoId=014788-3; Sequence=VSP_006446;
TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, we spleen, peripheral blood Leukocytes, bone marrow, heart, placskeletal muscle, stomach and thyroid.
INDUCTION: Up-regulated by T cell receptor stimulation.
PTM: The soluble form of isoform 1 derives from the membrane by proteolytic processing. (By similarity). The cleavage may k catalyzed by ADAM17.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                               express mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL outhe European Bioinformatics Institute. There are no restricticuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.chor send an email to license@isb-sib.ch).
MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190; Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee
                                                                         receptor
                                                                                                                                                                             PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
                                                                                                                                                                                                                                   osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005164; F:tumor necrosis factor receptor binding;
GO; GO:0006955; P:immune response; NAS.
GO; GO:0030316; P:osteoclast differentiation; NAS.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
                                                                         factor
                                                                     necrosis factin Trells.";
                                                                                                                                                                              Nagai M., Kyakumoto S., Sato N.;
"Cancer cells responsible for humoral hypercalcemia encoding a secreted form of ODF/TRANCE that induces formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=014788-1; Sequence=Displayed;
Name=2; Synonyms=SODF;
IsoId=014788-2; Sequence=VSP_006447
                                                                    is a novel ligand of the tumor ivates c-Jun N-terminal kinase Chem. 272:25190-25194 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019047; AAB86811.1; --
EMBL; AF053712; AAC39731.1; --
EMBL; AB064269; BAB79694.1; --
EMBL; AB061227; BAB71768.1; --
EMBL; AB064270; BAB79695.1; --
EMBL; AF013171; AAC51762.1; --
EMBL; AB037599; BAA90488.1; --
HSSP; O35235; 1JTZ.
Genew; HGNC:11926; TNFSF11.
                                                                                                                                          (ISOFORM 2)
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                                                                                                                                          SEQUENCE FROM N.A.
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MEDLINE=20175237;
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MIM; 602642
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                                                                                                                                                        l superfamily
similarity).
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                                                                                                             Tumor necrosis factor ligand superfamily
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                                                                                                                                                 Tumor necrosis factor ligand superfar
member 11, soluble form (By similaris
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
Cleavage (By similarity).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform 3).
/FTId=VSP 006446.
Missing (in isoform 2).
/FTId=VSP 006447.
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Murinae; Mus
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rtokine; Differentiation; Glycoprotein;
Transmembrane.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Pred. No. 2.4e-12;
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Mus musculus (Mouse).
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MEDLINE=94185175; PubMed=7511063; I
Takahashi T., Tanaka M., Brannan C
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"Generalized lymphoproliferative
mutation in the Fas ligand.";
Cell 76:969-976(1994).
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SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; F
PROSITE; PS50049; TNF_2; 1
Alternative splicing; Cytc
Receptor; Signal-anchor; T
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317 AA;
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This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
       SEQUENCE FROM N.A.
                                                                                                                                                                                             Name=FagLS;
                                     STRAIN=BALB/c;
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Yagita H.;
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, a receptor that May be involved in cell development. le in the induction of ted suicide of mature tor TNFRSF6B/DCR3 TNF of llized tt two members 못. -8; 9 ಡ SEQUENCE FROM N.A. (ISOFORM FASLS).
STRAIN=C3H; TISSUE=Spleen;
MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: a new alternatively spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999). and membrane protein (isoform FASL); ¤ Ø Isold=P41047-2; Sequence=VSP 006445;
PTM: The soluble form derives From the membrane form by proteolytic processing (By similarity).
DISEASE: A deficiency in this protein is the cause of generallymphoproliferation disease phenotype (gld). Gld mice presentlymphadenopathy and autoantibody production. The phenotype is recessively inherited.
SIMILARITY: Belongs to the tumor necrosis factor family. MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106 Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; "The mouse Fas-ligand gene is mutated in gld mice and is part of family gene cluster."; MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016 gld mice." Okumur c. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).

FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor the transduces the apoptotic signal into cells. May be involved cytotoxic T cell mediated apoptosis and in T cell developme TNFRSF6/FAS-mediated apoptosis may have a role in the induct peripheral tolerance, in the antigen-stimulated suicide of T cells, or both. Binding to the decoy receptor TNFRSF6B/Dc modulates its effects (By similarity).

SUBUNIT: Homotrimer (Probable). Fenner M.H., Shioda T., Isselbacher K.J.; "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand amino acids."; "Polymorphism of murine Fas ligand that affects the biological other MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914 Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Oku Lowin B., VARIANTS ALA-184 AND GLY-218. STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. the Fas-ligand and CHARACTERIZATION OF VARIANT GLD.
MEDLINE=96091792; PubMed=7495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin Rousseau M., Bron C., Renno T., French L., Tschopp J.; "Characterization of the non-functional Fas ligand of Int. Immunol. 7:1381-1386(1995). Secreted (isoforms FASL and FASLS).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2; IsoId=P41047-1; Sequence=Displayed; of SUBUNIT: Homotrimer (Probable). SUBCELLULAR LOCATION: Type II m (ISOFORM FASL) SEQUENCE FROM N.A. (ISOFORM FASL) Peitsch M.J., Tschopp J.J.; "Comparative molecular modelling of the TNF family."; Mol. Immunol. 32:761-772(1995). Immunity 1:131-136(1994)

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ERBI, 106349; AAA13780.;

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DR RRB:, 1410364; AAA13780.;

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DR RRB:, 150535; AAB022106.1;

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N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform FasLS).
/FTId=VSP_006445.
T -> A (in strain BALB/c, strain DBA/l and strain DBA/2; enhances cytotoxicity).
E -> G (in strain BALB/c, strain DBA/1 and strain DBA/2; enhances cytotoxicity).
F -> L (in gld; abolishes binding of FASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n no way
commercial
                                                                                                                                                                                                                                               PSEQUENCE FROM N.A.

TISSUE=Lymphocytes;

MEDLINE=21383618; PubMed=11491535; DOI=10.1007/8002510100322;

MEDLINE=21383618; PubMed=11491535; DOI=10.1007/8002510100322;

Meiss W.R., Ansari A.A.;

Weiss W.R., Ansari A.A.;

"Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules.";

Immunogenetics 53:315-328(2001).

-I-FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3

modulates its effects (By similarity).

-I-SUBUNIT: Homotrimer (Probable).

-I-SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                               igand)
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PROSITE; PS00251; TNF 1; 1.

PROSITE; PS00251; TNF 1; 1.

PROSITE; PS0049; TNF 2; 1.

Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).

T CHAIN 129 280 Tumor necrosis factor ligand superfamil member 6, soluble form (By similarity).
                                                                                                                                                         Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                              antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family
                                                                                                               (FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (Potential).
Extracellular (Potential)
Pro-rich.
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                                                           (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
is factor ligand superfamily member
                                 280 AA
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Cleavage (
Potential.
                                                                                                                                            FASL;
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InterPro; IPR008064; Fas ligand.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
PRINTS; PR01681; FASLIGAND.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                           (CD95L protein).
Name=TNFSF6; Synonyms=CD95L,
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HSSP; P50591; 1D2Q.
                                STANDARD;
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28-FEB-2003
05-JUL-2004
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RESULT 14
TNF6_CERTO
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                                                                                                                                                                                                      YWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVA
                                                                                                                                                                                                                                                                                   -EWEDT-YGIVLLSGVKYKKGGLVINETGLYF
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                                                                                                                                                                                                                                                                   AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY
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                                                                            Length 280;
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Catarrhini; Hominidae; Homo
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location
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FAS
                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95071350; PubMed=7980502;
Mita E., Hayashi N., Iio S., Takehara T., Hijioka T.,
Fusamoto H., Kamada T.;
"Role of Fas ligand in apoptosis induced by hepatitis infection.";
                                                                                                                                                           , אסר T., Suda
chromosomal lor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF6 HUMAN STANDARD; PRT; 281 AA. P48023; Q9BZP9; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Tumor necrosis factor ligand superfamily member 6 (Apoptosis antigen ligand) (APTL) (CD178 antigen) Name=TNFSF6; Synonyms=APT1LG1, FASL;
                                                                                                                                                                                                                                                                                                                                                                                                                           278
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(GlcNAc.
(GlcNAc.
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                                                                                          4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95105731; PubMed=7528780;
Alderson M.;
"Fas ligand mediates activation-induced cell
                                                                              DB
                                                                                                 d. No. 4e-1
Mismatches
                                                                           Score 187;
Pred. No. 4
N-linked
N-linked
N-linked
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MEDLINE=95127560; PubMed=7826947;
Takahashi T., Tanaka M., Inazawa J.
"Human Fas ligand: gene structure,
specificity.";
                                                                                                                                                                                                                                                                                                 -KPNSRSMPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . (ISOFORM 1).
PubMed=7528780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6:1567-1574 (1994)
                                                                                                          26;
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                                              MW;
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Mammalia; Eutheria; Primates;
                                                                           12.7%;
22.1%;
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95) to the
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183
249
259
31407
                                                                                                          Conservative
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Schaetzlein C.E., Poe
Submitted (JUN-1995)
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                                                                                          Similarity
61; Conserv
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TISSUE=Leukocyte;
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183
249
259
280 AA;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                               AHLTG
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CARBOHYD
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SEQUENCE
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Tanaka M., Itai T., Adachi M., Nagata S.;
Tanaka M., Itai T., Adachi M., Nagata S.;
"Downregulation of Fas ligand by shedding.";
"Downregulation of Fas ligand by shedding.";
Nat. Med. 4:31-36(1998).
-!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects.
                                                                                                                                                                                                                                                                                                                                                                                    S.d.,
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                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gabbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length hum
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Zeytun A., Nagarkatti M., Nagarkatti P.S.; "Isolation and characterization of a new naturally occuring varihuman Fas ligand that is expressed only in membrane bound form." Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein. May be releainto the extracellular fluid, probably by cleavage form the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: Defects in TNFSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS) [MIM:601859]; also known Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
PTM: N-glycosylated.
PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      MILKINGON 9.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequences.";
Acad. Sci. U.S.A. 99:16899-16903(2002)
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Name=1;
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DISEASE: Defects in TNFSF6 are
lymphoproliferative syndrome (A
                                                                                                                                                                                          (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS
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SUBUNIT: Homotrimer
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                                                                                                                                                                                         FROM N.A.
                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
                                                                                                                                                                                                            TISSUE=Blood
                  "Isolation human Fas 1 Submitted (
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                                                                                                       SEQUENCE F
Wilkinson
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collaboration
                                                                                                                                                                      in no way
commercial
                                                                                                                                                                                      removed. Usage by and for commercial ent (See http://www.isb-sib.ch/announce/
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor ligand superfamily member 6, membrane form.

Tumor necrosis factor ligand superfamily member 6, soluble form.

Cytoplasmic (Potential).

Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALMA, 901839; -.

R GO; GO: 0005887; C: integral to plasma membrane; TAS.

R GO; GO: 0005102; F: receptor binding; TAS.

R GO; GO: 0007267; F: receptor binding; TAS.

R GO; GO: 0007267; F: recell-cell signaling; TAS.

R GO; GO: 0007165; P: signal transduction of I-kappaB kinase/NF-k. . .; I GO; GO: 0007165; P: signal transduction; TAS.

R GO; GO: 0007165; P: signal transduction; TAS.

R InterPro; IPR008064; Fas ligand.

R InterPro; IPR0080653; TNF family.

R InterPro; IPR0080983; TNF family.

R InterPro; IPR0080983; TNF like.

R PRINTS; PR01234; TNECROSISFCT.

R PRODOM; PD002012; TNF subf; 1.

R PRODOM; PD002012; TNF 1; 1.

R PROSITE; PS50049; TNF 2; 1.

R Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

R Signal-anchor; Transmembrane.

CHAIN 1 281 TUMOR DESCRIPTION TO THE TO 
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(GlcNAc. . .) (Potential).
(GlcNAc. . .) (Potential).
SSL -> ATPVHPLKKRS (in isoform
                lymphadenopathy and splenomegaly.
SIMILARITY: Belongs to the tumor necrosis factor family.
DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm"
   with massive
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abolishes cytotoxity.
F->L: Abolishes binding to
    thrombocytopenia
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Poly-Pro.
Cleavage.
Potential.
N-linked (
N-linked (
    anemia and
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EMBL; U08137; AAC50071.1; -.
EMBL; U11821; AAC50124.1; -.
EMBL; D38122; BAA07320.1; -.
EMBL; AF288573; AAG60017.1; -.
EMBL; Z96050; CAB09424.1; -.
EMBL; BC017502; AAH17502.1; -.
EMBL; AB013303; BAA32542.1; -.
PIR; I38707; I38707.
HSSP; P50591; 1D2Q.
Genew; HGNC:11936; TNFSF6.
H-InvDB; HIX0001337; -.
MIM; 134638; -.
MIM; 601859; -.
nvolving hemolytic
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cytotoxicity

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61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
                                                                                                         ---- 146
                                   86;
                Query Match
12.6%; Score 186; DB 1; Length 281; Best Local Similarity 22.1%; Pred. No. 4.9e-07; Matches 63; Conservative 54; Mismatches 82; Indels
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(c) 1993
       Copyright
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sw model using search, protein OM protein Search time 162 Seconds (without alignments) 670.862 Million cell up 2005, 11:54:33 ᠬ June Run on:

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281

..NEHLIDMDHEASFFGAFLVG

US-10-662-431-2 1478 1 MAMMEVQGGPSLGQTCVLIV.. score: Sequence:

Gapext BLOSUM62 Gapop 10.0 Scoring table:

0.5

residues 2105692 seqs, 386760381 Searched:

55 of hits satisfying chosen parameters Total number

seq seq 0B 0B Minimum Maximum

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Post-processing: Minimum Match 100% Maximum Match 100% Listing first 500 summaries

Database

A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

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Result		Query	•		!	•
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г г	47	100.0		7	AAW19777	Aaw19777 Novel cyt
7	47	0	œ	~	AAW27134	4 Human
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6 ABU714 6 ABG727 6 AAO295 6 ABU085 6 ABG719 6 ABG719 6 AAE362 6 AAE362 7 ADB614	7 ADC3520 7 ADD1408 7 ADD1901 7 ABW0227 8 ADE7695 8 ADK7231 8 ADK7230	8 ADK7231 8 ADJ6397 8 ADL7181 8 ADK1549 8 ADK1549 8 ADK1420 8 ADK8221 8 ADS8800 8 ADS8800
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ALIGNMENTS

Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy. label= Glycosylation note= "putative N-linked glycosylation site" /label= Extracellular_region 109 = Transmembrane_region 1. .14 /label= Cytoplasmic_region 15. .281 /note= "Claim 3" 15. .40 /label= Transmembrane_region Location/Qualifiers Æ "Claim 4" 11. .281 'note= "Claim 2" note= "putative 14. .281 note= "Claim 1" AAW19777 standard; protein; 281 97WO-US000272. cytokine Apo-2 ligand (first entry) 1. .281 /note= " Modified-site WO9725428-A1. Homo sapiens 08-JAN-1997; 17-JUL-1997. 22-SEP-1997 AAW19777; Key Peptide Protein Protein Protein Region Region Region Novel RESULT 1 AAW19777

for

develop products, tumours, graft

used to der diseases, 1

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The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand superfamily. The products can be used in the diagnosis and treatment of disorders related to under-expression, over-expression or altered expression of AIM-I. AIM-I or agonists can be used for treating autoimmune disorders including systemic lupus erythematosus, immunoproliferative disease lymphadenopathy (IPL), angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis, chaptes, and multiple sclerosis, graft versus host disease, to inhibit neoplasia such as tumour cell growth, to treat restenosis, to regulate haematopoiesis in endothelial cell development, to stimulate peripheral collerance and cytotoxic T-cell mediated apoptosis. Antagonists can be used for treating cachexia, cerebral malaria, rheumatoid arthritis or osteoporosis, for preventing graft-host rejection, and as anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 3.8e-137
Mismatches 0
                                                                                                                                              New isolated apoptosis inducing molecule-I - the diagnosis and therapy of e.g. autoimmune versus host disease or inflammation.
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Best Local Similarity 100.
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N-PSDB; AAT85210.
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  14-MAR-1996;
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uring cells
nucleic
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                                                                                                                                                                                               A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 41 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                TACFLKE
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                                                                                                                                                                                                                                                                                                                                                                         Score 1478; DB 2;
Pred. No. 3.8e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis inducing molecule-I; AIM-I; autoimmune tumour necrosis factor ligand superfamily; AIM-I neoplasia inhibition; anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AIM-I)
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100.0%; Pr
                                                                                                                                                                       Claim 4; Fig 1a; 72pp; English.
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             96US-00584031
                                                                Chuntharapai
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100
1; Conservative
                                      GENENTECH INC
                                                                                         WPI; 1997-372867/34
N-PSDB; AAT72796.
                                                                                                                                                                                                                                                                                                                                                281 AA;
                                                                                                                                  cytokine,
                                                                                                                                             apoptosis for
                                                                 AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9733899-A1.
            09-JAN-1996;
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Best Local Simi
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                                                                Ashkenazi
                                                                                                                                                                                                                                                                                                                                                Sequence
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AAW27134
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reatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAW19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281;
                                                                                                                  receptor-binding region"
                                                                                                                               = "potential KEX2 protease processing .111
                                                                                                                                                                                   KEX2 protease processing
                                                                                                                                                                                                                                                                                                                                                                                 TRAIL, a novel cytokine, induces apoptosis in cancer and cells - useful for treating thrombotic microangiopathy, cinfection and for use in assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                           = "potential N-glycosylation site"
.150
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Pred. No. 3.8e-137;
Mismatches 0;
                                                                                   Transmembrane_domain
                                                                Cytoplasmic_domain
                                                                                      /label=
/label= Extracelular_c
/~~te= "contains a rec
therapy
                                                                                                                                                                                                                                                                                                                                                                                                                            43-44; 62pp; English.
                                          Location/Qualifiers
                                                                                                                                                                                  "potential
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95US-00548368
thrombotic microangioplasty;
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/label=
                                                              label=
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-118715/11
N-PSDB; AAT72847.
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281; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microangiopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
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                                                                                                                             Cleavage-site
                                                                                                                                                   Modified-site
                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                        WO9701633-A1.
                      Homo sapiens
                                                                                                                                                                                                                                              25-JUN-1996;
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01-NOV-1995
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Best Local S
Matches 281
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TR6; tumour necrosis factor related receptor; human; treatment; stroke; inflammation; arthritis; septicaemia; autoimmune disease; restenosis; transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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3.8e-137;
se 0;
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 32-33; 34pp; English.
                                                                                                       281
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97US-00853684.
97US-00916625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                97EP-00310562
                                                                                                       protein;
                                                                                                                                                                     entry)
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polypeptide, antibody,
                                                                                                                                                                   (first
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B; AAV63096.
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                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1998.
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09-MAY-1997;
22-AUG-1997;
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241
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of
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cytokine TNF-related apoptosis ligand polypeptides g recombinant polypeptides for research and therapy ymphoma, melanoma and viral infections.
                                                                                                                                                                                                                             resear
                                                                                                                                                                                                                          Tumour necrosis factor related apoptosis ligand; TRAIL; cytokine; therapy; leukaemia; lymphoma; melanoma; viral
                                                                        281
                                                                                           281
                                                                                                                                                                                                                                                                                                  domain"
                                                                       Score 1478; DB 2;
Pred. No. 3.8e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                 cytoplasmic
                                                                                                                                                                                                                                                                                                                     "transmembrane region"
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39. .281
'--- "extracellular d
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                 "N-terminal
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95US-00548368
                                                                                                                                             standard; protein;
                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      producing recombinant
                                                                                                                                                                                                                                                                                                          .38
                                                                                                                                                                                                         Human TRAIL polypeptide
                                                                                                                                                                                                                                                                                         1. .18
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-347322/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding
                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1995;
01-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RG,
                                                                                                                                                                                     05-AUG-1998
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                               181
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            121
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Best Local S
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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteoporosis, osteomyelitis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat homber of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosupressive agents. Host cells, produce recombinant AGP-1
                                                                                                                                                        240
                                                                                                                                                                                  240
                9
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation; bone resorption; haematopoietic disease.
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sacid encoding AGP-1, a tumour necrosis factor-related protein for treating inflammation, bone resorption and haematopoietic
                                                                                                                                                        FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                   281
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N-PSDB; AAV15295.
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N-PSDB; AAX86987.
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in mammalian cancer
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5-APR-1998;
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                                                   Query Match
Best Local
Matches 28
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ptides can
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                                                                                                        VRERGPO
                                                                                                                           VRERGPO
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nd a
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                                                                                                                                                DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSETISTVQEKQQNISPL
                                                                                                                   Protein associated with neurodegenerative and autoimmune disea
                                                              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSG
                     281;
                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory apoptotic;
                                          Indels
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                   No. 3.8e-137;
Mismatches
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lupus erythematosus; rhuematoid arthritis; SEP;
surface receptor; TRAIL protein.
                     Score 1478;
Pred. No. 3
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                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorder
                                                                                                              DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                       DB 2;
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glomerular nephritis;
                                                     Score 1478;
Pred. No. 3.8
; Mismatches
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or cells.
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98US-00060533
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                                                                    Similarity 100
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lupus; immune-mediated g
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                                                                                   Сарв
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  nd screening
treating di
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 and
coding sequence can also be used in quantitative ar
techniques. Anti-Apo-2L antibodies can be used for
associated with increased apoptosis
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                                                            Score 1478; DB 2;
Pred. No. 3.8e-137;
Mismatches 0;
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N-PSDB; AAA07425.
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assays for Apo-2 ligand, e.g. detecting its expression in specific cells tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand-induced apoptosis, may be employed to treat pathological conditions or diseases associated with increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
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Pred. No. 3.8e-137;
Mismatches 0;
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99US-0162506P.
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the growth of tumors in
polypeptide activity or
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N-PSDB; AAC58120.
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Best Local Similarity
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                                                                                     Sequence 281 AA;
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01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
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                            The present invention describes an antibody that binds to a human protein (1) selected from: PRO181; PRO1269; PRO1410; PRO175; PRO1780; PRO4334; PRO1927; PRO155; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397; PRO1927; PRO155; PRO1096; PRO2038; and PRO2262. (1) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (1) can also be detected to diagnose tumours. Agents which inhibit the activity of (1), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (1), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (1). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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TNF related apoptosis-inducing ligand; tumour cell;
TRAIL receptor ligand; solid tumour; carcinoma; mammary
non-small cell lung carcinoma.
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Pred. No. 3.8e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a human TRAIL polypeptide
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            226pp; English
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                                                                                                                                                The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
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                             and
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Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid diepoxide tumor necrosis factor related apoptosis-inducing ligand.
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Pred. No. 3.8
; Mismatches
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                                                                                                  Disclosure; Page
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                                                                                                                                                                                                                                                                                                                                                                              lung carcinoma)
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disorders.
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                                                                                                                          protein.
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                                                                                                                    The present sequence is human AGP-1, a type II transmembrane protection proteins comprising an Fc immunoglobulin region fused to the Fusion proteins can be used to induce apoptosis in a tissue, and to treat proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced discretive disorders include cancers, such as breast, prost lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders be autoimmune disorders or transplant rejection. Cardiovascular discuch as arteriosclerosis may also be treated. The AGP-1 containing proteins have increased biological activity compared to the solubly proteins used in prior art therapies
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                                                                                  region, used to trea and virally-induced
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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                                                                                of AGP-1 protein and an Fc adisorders,
                                                                                                          2; 93pp; English.
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                                                        WPI; 2000-665240/64
N-PSDB; AAC67831.
                                                                                                                                                                                                                                                            Similarity
                        INC
                                                                                                                                                                                                                                    Sequence 281 AA;
                                                                                 Fusion protein
proliferative
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                        AMGEN
                                                                                                         Claim 3; Fig
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        6-APR-1999
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The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful
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Pred. No. 3.8e-137;
Mismatches 0;
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WI;
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Wood
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Watanabe CK,
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                              99WO-US012252.
99US-0141037P.
99US-0144758P.
99WO-US020111.
99WO-US020594.
99WO-US028313.
99WO-US028634.
99WO-US028634.
99WO-US028634.
99WO-US028634.
99WO-US028631.
99WO-US028631.
200WO-US03099.
200WO-US003565.
200WO-US004341.
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2000WO-US006884.
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 2000WO-US014941
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31; Conservative
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N-PSDB; AAC91579.
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                               02-JUN-1999;
22-JUN-1999;
20-JUL-1999;
01-SEP-1999;
08-SEP-1999;
30-NOV-1999;
02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
16-DEC-1999;
16-DEC-1999;
16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
16-DEC-1999;
17-MAR-2000;
17-MAR-2000;
15-MAR-2000;
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30-MAY-2000;
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Shelton DL,
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Best Local Sim
Matches 281;
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cytostatic; virucide; cancer; viral infection; gene therapy; lymphoma;

(TRAIL)

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domain

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Location/Qualifiers
1. .18
/label= N_terminal_cytoplasmic_dc
19. .38
/label= Transmembrane_region
39. .281
/label= Extracellular domain
                                                                                         Human; tumour necrosis factor; TNF; cytokine; TNF related apoptosis inducing ligand; TRAIL; human immunodeficiency virus; HIV; leukaemia;
                                                                           apoptosis inducing ligand
                                                                                                                                                                                                                                                      95US-00496632.
95US-00548368.
96US-00670354.
98US-00048641.
                                                                                                                                                                                                                                         99US-00320424
                              standard; protein;
                                                            entry)
                                                                                                                                                                                                                                                                                                                    Goodwin RG;
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N-PSDB; AAD18395.
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01-NOV-1995;
25-JUN-1996;
26-MAR-1998;
10-NOV-1998;
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                                                            18-DEC-2001
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                                            AAE11031;
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Best Local S
Matches 281
                                                                                                                 melanoma.
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                              AAE11031
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                                                                                                                                cancer
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                                                                                                                                                                                                                                                                              Use of divalent metal ions for making Apo-2 ligand and in i
containing Apo-2 ligand for increasing yield and stability
trimers, useful for therapeutic applications.
                                                                                                                                                                                                                                          Leung
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              Score 1478; DB 4;
Pred. No. 3.8e-137;
Mismatches 0;
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Simmons
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Pai R, Shahrokh Z,
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                                                                    protein;
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                                                                   standard;
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nes 281; Conser
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                                                                                                                                               Homo sapiens
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O'connell
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ID AAB67243
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The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
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Pred. No. 3.8e-137;
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larity 100.0%;
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The invention relates to a human tumour necrosis factor (TNF) related receptor, TR6. TR6 can be expressed by standard recombinant methodology.

The TR6 polypeptides are useful for treating chronic and acute inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. chost disease, infection, stroke, ischaemia, acute respiratory disease. Syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis, and Alzheimer's disease. These may also be used to inhibit production of TNF-alpha and eicosanoids, as research reagents and materials for discovering treatments and diagnostics to animal and human diseases. The polypeptides may further be used as immunosens to produce antibodies immunospecific for the TR6 polypeptides. The polymucleotides may also be used as hybridization probes for cDNA and genomic DNA, for isolating full-length cDNAs and genomic clones encoding TR6 and of other
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bone
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                                MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                               RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                              FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                            AAB48350 standard; protein;
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genes having high sequence similarity to TR6 gene, and for chromosome identification. The present sequence represents a human TL2 polypeptide TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and a ligand for the TL2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating an individual at risk for or sufferir from infection with a pathogenic or opportunistic organism. The method involves administering a combination of two to five agents comprising:
                                                                                                                                      MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                       DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                                                                  DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor and antigen-specific T cells.
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                                                                                      Length 281;
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fungicide; protozoacide; virucide; anti-inflammatory; a
tuberculostatic; cytostatic; human; TRAIL.
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                                                                                    Score 1478; DB 4;
Pred. No. 3.8e-137;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 281; Conservative (
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Thomas EK;
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c (a) dendritic cell mobilisation factor; (b) dendritic cell maturation agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; or (e) activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. T. cruzi, which causes Chaga's disease). The methods are especially useful for treating an individual suffering from immunosuppression by enhancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammations, chickenpox, oral or genital entres, multifocal leukoencephalopathy, hepatitis, AIDS, T cell leukemia or T cell lymphoma. The activated antigen-presenting dendritic cells are useful as a vaccine adjuvant. The present sequence represents a human TRAIL polypeptide fragment
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                                                                                                              The present invention relates to a new method for treating a tumourbearing subject. The method involves administering a combination of 2 to 5 agents comprising dendritic cell mobilisation factor, dendritic cell maturation agent, tumour-killing agent, T cell enhancing factor or activated, antigen-specific T cells. The method is useful for treating tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or cervical intraepithelial neoplasia. The present amino acid sequence represents the human TRAIL protein that was used in the method of the
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                          cancers, e.g. liver cancer or lof dendritic cell populations, antigen-specific T cells.
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                          Treating an individual with tumors or tumor, by administering a combination cell enhancing factors and activated,
                                                                                      Disclosure; Page 41-43; 44pp; English
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                                                                                                       novel method for
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100.0%; Pred. No. 3.8
:ive 0; Mismatches
                                                                       Use of a synergistic combination of death diterpenoid triepoxides for killing of tun
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                                                                                          17-20; 20pp; English.
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              Apo-2 ligand; Apo-2L; antitumour; therapy.
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                                                                                                                                                                                                                                         cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid upus erythematosus, lichen planus. The combination may be administered with other agents. The potent synergy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human TNF related apoptosis inducing ligand (TRAIL) protein sequence. TRAIL is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to
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                                                                                                                                                                                                                                enhanced killing
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The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The invention relates to methods of inducing apoptosis in mammalian cells, and especially to the use of Apo-2L receptor agonists and CPT-11 (a chemotherapeutic agent of the topoisomerase I inhibitor class) to synergistically induce apoptosis in mammalian cells, in particular mammalian cancer cells, and especially colorectal cancer cells (claimed). The cells may be in cell culture or in a mammal, e.g. a mammal suffering from cancer or a condition in which induction of apoptosis in the cells is desirable. A claimed method of treating cancer in a mammal comprises administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is administered about 6-72 hours prior to administration of the Apo-2L receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L ceptor antibodies. Exposure of the cancer cells to CPT-11 and Apo-2L receptor antibodies. Exposure of the cancer cells to CPT-11 and Apo-2L receptor antibodies to upregulation of DR4 and DR5 receptors, directing the cells towards an apoptotic pathway rather than cell cycle arrest and possible DNA repair, thus providing enhanced antitumour activity. An example illustrates the synergistic inhibition of tumour growth by Apo-2L and CPT-11 in athymic nucle mice injected s.c. with human contacts and contacts. ö cancer; tumour; on of tumour s.c. with human 120 9 9 ${\color{red} H}$ 18 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE of CPT-11 which is a chemotherapeutic agent of the topoisomerase bitor class, and Apo-2 ligand receptor agonist for enhancing tosis in mammalian cells, or for treating cancer in a mammal. Gaps Claim ; 0 281; of in method colorectal Length Indels Score 1478; DB 5; Pred. No. 3.8e-137; 0; Mismatches 0; "Apo-2L polypeptide used TRAIL; human; apoptosis; Xiang H; Claim 18; Page 79-80; 84pp; English. Location/Qualifiers 114. .281 SK, 100.0%; Sc 100.0%; Pr 0; COLO205 colon carcinoma cells Kelley 2001WO-US023691 2000US-0221256P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an Escherichia coli strain (I) deficient in chromosomal degp and prc encoding protease Degp and Prc, respectively, and harbouring a mutant spr gene, the product of mutant spr gene suppresses growth phenotypes exhibited by strains harbouring prc mutants. (I) is useful for producing a polypeptide, by culturing (I) comprising nucleic acid encoding the polypeptide, which is heterologous to the strain, such that the nucleic acid is expressed, and recovering the heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor under conditions of high- or low-cell density fermentation. The polypeptide is an antibody (humanised or full-length antibody) or Apo2 ligand. The antibody (humanised or full-length antibody) or Apo2 ligand. The antibody is an anti-vascular endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2, anti-CD20, anti-CD40, or anti-CD11 antibody is an antibody fragment thaving a light chain (kappa light chain). The antibody fragment thaving a light chain (kappa light chain). The antibody fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-cD18 Fab'2-leucine zipper fusion with a 6-histidine factom the present fusion with a 6-histidine factom the present fusion with a 6-histidine factom fab'd fusion fusion fab'd fusion fusion fusion factor fab'd fusion fusion fab'd fusion
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anti-CD18
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                                                                                                                                                                                                                                                                                                                                               antibody;
nti-CD20;
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3F Fab.
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prc m
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sequence SEQ ID NO:4
                                                                                                                                                              standard; protein; 281
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N-PSDB; ABQ73920.
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                                                                                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                       RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                        Producing a population of activated, Cryptococcus neoformans antigen-
presenting dendritic cells for preventing or treating C. neoformans
infection comprises causing the obtained dendritic cells to present t
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3.8e-137;
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Pred. No. 3.8
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                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                      Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26.
        DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                            LVIHEKG
                                                                        RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKS
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== "TNF domain"
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KHOSRAVI
SAVITZKY
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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tummour necrosis factor (TNF)-related apoptosis inducing cliquad (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

Apoptosis is induced by certain cytckines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-21). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors. DR4 and DR5, as well as two decoy receptors, DR4 and DR5, as well as two decoy receptors, DR2 interferons, induces apoptosis in tummour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the naturally occurring splice variants may differ in the cellular distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a main antagonists). Pharmaceutical compositions, comprising the level of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which cannon ocid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products autoimmume diseases. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products autoimmume diseases, diseases involved in the non-normal devenue presented 
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red. No. 3.8e-137;
Mismatches 0;
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Alzheimer's disease; Parkinson's disease; amyotrophic lateral smultiple sclerosis; retinitis pigmentosa; cerebellar degeneratiaplastic anaemia; myocardial infarction; stroke; reperfusion intoxin-induced liver disease; cancer; lupus; herpes virus infect
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Homo sapiens

domain" "Transmembrane Location/Qualifiers .40 'note= Domain Domain

281 == "Extracellular domain" "N-glycosylated" /note= 109 note= Modified-site

US6462176-B1

08-OCT-2002

97US-00928069 11-SEP-1997; 96US-0026943P 23-SEP-1996;

GENENTECH INC (GETH)

Ashkenazi AJ;

WPI; 2003-173840/17 N-PSDB; ABX15469.

ation Novel isolated Apo-3 polypeptide useful for inducing apoptosis mammalian cells, for generating antibodies, in affinity purific techniques, and in competitive-type receptor binding assays.

52pp; English 4, 4; Fig Example

The invention relates to an Apo-3 polypeptide having an extracellular domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumourn necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising receptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 tused to a heterologous amino acid sequence. The Apo-3 polypeptide is useful therapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis has been associated with conditions such as cancer, lupus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial infarction, stroke, reperfusion injury, and toxin-induced liver disease. The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating antibodises, as standards in assays for Apo-3, in affinity punifications and in competitive-type receptor binding assays. The chimeric rechniques, and in competitive-type receptor binding assays. The chimeric App-3 antibodises. The present sequence represents polypeptide sequence represents polypeptide sequence of the human Apo-2 ligand protein which is also reported to be involved in apoptotic cell death. In the current invention the apoptotic activity of the human Apo-2 ligand protein was measured on human lymphoid cells erating fication the chimeric sequence of nvolved in oplications such which samples

Sequence 281 AA;

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  281;
 Length
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ore 1478; DB 6;
red. No. 3.8e-137;
Mismatches 0;
Score 1478;
Pred. No. 3.
100.0%; S. larity 100.0%; P. Conservative 0;
        Similarity
                 281;
Query Match
Best Local S
Matches 281
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8

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RESULT 25 ABU10205

standard; protein; 281 **ABU10205**

ABU10205;

entry) (first 11-AUG-2003

Human Apo-2 ligand.

Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; neurodegenerative disease; immunosuppresive; tissue typing.

Homo sapiens

US2003004313-A1.

02-JAN-2003

2002US-00112193 28-MAR-2002;

96US-0026943P 97US-00928069 23-SEP-1996; 11-SEP-1997;

(GETH) GENENTECH INC

Ashkenazi AJ;

WPI; 2003-438872/41 N-PSDB; ACA61696.

vivo r inducing or for in or for stimulating on e.g. cancer cells, New isolated Apo-3 polypeptides, useful for apoptotic activity in mammalian cells, e.g. or ex vivo gene therapy techniques.

Example 4; Fig 4; 50pp; English.

The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/inflammatory effects of Apo-3 resulting from NF-kappaB activation. The nucleic acid sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-2 ligand

Sequence 281 AA;

ö Gaps . 0 Length Indels Score 1478; DB 6; Pred. No. 3.8e-137 0; Mismatches 0; ; 0 100.0%; |larity 100.0%; | Conservative Query Match Best Local Similarity Matches 281; Conser

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Wood
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Watanabe CK,
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99US-0115554P.
99US-0115558P.
99US-0116533P.
99US-0116533P.
99US-0116533P.
99US-0123618P.
99US-0123618P.
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99US-0123618P.
99US-0123618P.
99US-0123618P.
99US-01012252.
2000WO-US0124291.
2000WO-US01252P.
99US-0141037P.
99US-014042.
2000WO-US013699.
2000WO-US01736.
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N-PSDB; ACA58016.
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, Smith
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12-JAN-1999;

20-JAN-1999;

08-MAR-1999;

10-MAR-1999;

10-MAR-1999;

12-APR-1999;

20-APR-1999;

21-APR-1999;

22-JUN-1999;

22-JUN-1999;

23-JUN-1999;

23-JUN-1999;

24-APR-1999;

25-AUG-1999;

26-JUN-1999;

27-APR-1999;

27-APR-1999;

28-AUG-1999;

29-OCT-1999;

20-JUN-1999;

21-APR-1999;

22-JUN-1999;

22-JUN-1999;

23-JUN-1999;

24-AUG-2000;

25-AUG-1999;

26-JUN-2000;

27-APR-2000;

28-MAY-2000;

28-MAY-2001;

28-MAY-2001;

29-OCT-1999;

21-APR-2000;

21-APR-2000;

22-MAY-2000;

22-MAY-2001;

22-MAY-2001;

22-MAY-2001;

22-MAY-2001;

23-AUG-2001;

24-JUN-2001;

25-MAY-2001;

26-AUG-2001;

27-JUN-2001;

28-AUG-2001;

29-AUG-2001;

29-AUG-2001;
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DAEYGLY
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                                                                                                               281
                                                                                                                                                SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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98US-0079689P.

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98US-0085149P.

98US-0087607P.

98US-0096891P.

98US-0096891P.

98US-0096894P.

98US-0096894P.

98US-01068824.

98US-0100263P.

98US-0100390P.

98US-0101476P.

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98US-0101476P.
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                                           DDSYWDPNDEESMNSP
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27-MAR-1998;
24-APR-1998;
29-APR-1998;
12-MAY-1998;
12-MAY-1998;
11-JUN-1998;
11-JUN-1998;
17-AUG-1998;
17-AUG-1998;
10-SEP-1998;
14-SEP-1998;
16-SEP-1998;
15-SEP-1998;
15-SEP-1998;
15-DEC-1998;
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The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, gastric, pancreatic, vulval, thytoid, central nervous system cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide or the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergic disease; allergy; TNF; TRAIL; diagnosis; necrosis factor-related apoptosis inducing ligand; skin inflammation.
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Pred. No. 3.8e-137;
Mismatches 0;
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 inflammatory,
                                                       32; Fig 54; 186pp; English
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hypothalamic,
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                                                                                                                                                                                                                                             (TNF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer; hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disorder, myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 3.8e-137
Mismatches 0;
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screening agents for allergic
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N-PSDB; ABX13715.
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The invention relates to antibodies that immunospecifically bind to tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptors (TRAIL-R). Antibodies of the invention are useful for treating, preventing or ameliorating cancer (e.g. cancers of pancreas, uterine, breast, colon, lung and gastrointestine and Kaposi's sarcoma) and other cast, colon, lung and gastrointestine and Kaposi's sarcoma) and other carrier disease, Alzheimer's disease and Huntington's disease), autoimmune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, Hashimoto's disease and immunodeficiency syndrome; AlDS, herpes viral infections and other viral rheumatoid arthritis), infectious diseases (e.g. acquired immune disorders disease, spendrome; AlDS, herpes viral infections and other viral infections), myelodysplastic syndromes (e.g. aplastic anaemia), graft-cufections, myelodysplastic syndromes (e.g. aplastic anaemia), graft-cufections), myelodysplastic syndromes (e.g. aplastic anaemia), graft-cufections, cerebrovascular disorders, thrombotic microangiopathies, disorders, cerebrovascular disorders, thrombotic microangiopathies, and ulcerative colitis and for wound healing. The invention is also used the prepare vaccines. The present sequence is human TRAIL protein also
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infectious diseases; myelodysplastic syndrome; cardiovascular (graft-versus-host disease; toxin-induced liver disease; cachex: cerebrovascular disorder; thrombotic microangiopathy; aplastic ischaemic injury; anorexia; diabetes; ulcerative colitis; psor: asthma; AIDS; therapy; TRAIL receptor; TRAIL-R; AIM-I.
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preventing, treating and ameliorating cancers and other
hyperproliferative disorders, binds immunospecifically t
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07-MAY-2002;
15-AUG-2002;
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                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                              20"
                                                                                                                                                                                                      Human; TNF related apoptosis inducing ligand; TRAIL; tumour necrosis factor; apoptosis; haemostatic; immunosuppressive; antilnflammatory; dermatological; thrombotic microangiopathy; thrombotic thrombocytopaenic purpura; TTP; HUS; SLE; clotting disorder; adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS; systemic lupus erythematosus.
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96US-00670354.
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01-NOV-1995;
25-JUN-1996;
26-MAR-1998;
10-NOV-1998;
26-MAY-1999;
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invention relates to compositions comprising heterotrimeric
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tumor necrosis factor (TNF) ligand family, and a second differe
of TNF ligand family, useful for treating cancer, osteoporosis
The antibody is useful for treating disorders mediated or exact TRAIL, e.g. thrombotic thrombotic thrombocytopaenic purpura (TTP), adult haemolytic uraemic syndi (even though it can strike children as well) small blood vesseldisorders e.g., cardiac problems in paediatric AIDS patients allupus erythematosus (SLE). The present sequence represents human
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Pred. No. 3.8e-137;
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          the detection, prevention and treatment of disease. In one embodiment, the detection, prevention and treatment of disease. In one embodiment, the heterotrimeric complex comprises full-length or extracellular portions of other TNF ligand family members, preferably RANKL. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer or osteoporosis, and particularly for inhibiting cancer cell proliferation, increasing B cell proliferation, or inducing apoptosis of T cells. A claimed method of inducing apoptosis of T cells. A heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha, lymphotoxin-beta or TRAIL. A claimed method of inhibiting cancer cell proliferation involves administering a heterotrimeric complex consisting of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis comprises administering an antibody against a complex comprising RANKL and TRAIL
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Pred. No. 3.8e-137
Mismatches 0;
ligand family
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The invention relates to an isolated antibody comprising a first amino acid sequence having 95 % identity to a second amino acid sequence of either variable heavy chain or light chain-complementarity determining regions (VHCDR1)/HCDR1, VHCDR2/VLCDR2 or VHCDR3/VLCDR3 appearing as ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that propertied or detecting, diagnosing, prognosing or arthogological propertied or detecting, diagnosing, prognosing or monitoring cancers, and other hyperpooliferative disorders) using the antibodies, a hybridoma cell line selected from the hybridoma cell lines contained in ATCC Deposit No. PTA-1319, PTA-2687, PTA-1369, PTA-2730, PTA-2369, 
                                                                                                                                                                                                                                                                                                          amino acid sequence having identity to other amino acid seques
either variable heavy/light chain-complementarity determining
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2000US-0246612P.
2000US-0248847P.
2000US-0252904P.
2001US-0295018P.
2001US-0327359P.
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                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                   Novel antibody for treating,
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GVHD; APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; TRAIL; tumour necrosis factor. TRAIL 281 necrosis factor standard; protein; (first entry) Human tumour 28-MAR-2003 ABP60546; ABP60546 ABP60

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WO200294192-A2 28-NOV-2002

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2002WO-US016106. 22-MAY-2002;

2001US-0293100P INC SCI (HUMA-) HUMAN GENOME 24-MAY-2001;

Ruben SM;

2003-156740/15

oody that immunospecifically binds tumor necrosis for treating, preventing or ameliorating Non-multiple myeloma, rheumatoid arthritis or Sjogren' Novel isolated antibody factor delta, useful for Hodgkin's lymphoma, mult

Disclosure; Page 216-217; 225pp; English

syndrome.

The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).

The antibody of the invention has dermatological, immunosuppressive, antishlammatory, antirhemmic, antibarthritic, cytostatic, antianaemic, antiallergic, antirhemmic, antiparthritic, cytostatic, antianaemic, tuberculostatic, antidabetic, natiparthritic, cytostatic, antianaemic, antiallergic, antidabetic, antiparthritic, ophthalmological, tuberculostatic, antidabetic, antibactic, antiparthritic, antiparthritic, antianaemic, antianteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.

The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in human, disease or disorder such as autoimmune disease, and graft versus cythematosus, rheumatoid arthritis or Sjogren's syndrome. The autibody is useful for detecting, disgnosing, prognosing, treating, preventing or ameliorating a disease or disorder associated with aberrant APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL receptor allergic encephalomyelitis, myocarditis, multiple sclerosis, dermatitis, asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis, uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as mysathenia stravis diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and proliferative disorders (e.g. leukemia). The present sequence represents

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TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;

Myperproliferative disorder; neurodegenerative disorder; immune disorder;

Myperproliferative disorder; neurodegenerative disorder; immune disorder;

Myperproliferative disorder; neurodegenerative disorder;

Myperproliferatis parkinson's disease; Hashimoto's thyroiditis;

Myperproliferatis; multiple sclerosis; Sjogren's syndrome; asthma;

Myperprolifery cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;

Mypolymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;

Myperproliferative disorder; myelodysplastic syndrome; viral infection;

Mypolymyositis; inflammatory disorder; myelodysplastic syndrome; aplastic anaemia;

Mypolymyositis; stroke; cardiovascular disorder; peripheral artery disease;

Mypore proliferative disorder; peripheral artery disease;

Mypolymyositis; arrhythmia; congestive heart failure; neovascularisation;

Mypore proliferation;

Mypore proliferation; human.
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                     Score 1478; DB 6;
Pred. No. 3.8e-137;
Mismatches 0;
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2001US-02949B1P.
2001US-0309176P.
2001US-0323807P.
2001US-0327364P.
2001US-0331044P.
2001US-0331310P.
2001US-0341237P.
2002US-0369860P.
                    Match 100.0%; Local Similarity 100.0%; les 281; Conservative
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07-NOV-2001;
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The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating, preventing or ameliorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or cantral nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and cheeting, preventing or ameliorating cancers and other hyperprolating to ameliorating neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease, retinitis pigmentosa, cerebellar degeneration and Huntington's disease, polymyositis, immune-related glomenloophicitis, multiple sclerosis, sjoyren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, immune-related glomenloophicitis, multiple sclerosis, polymyositis, immune-related glomenloophicitis, multiple sclerosis, infectious diseases (e.g. asthma, allergic disorders and rheumatoid arthritis), infectious diseases (e.g. acquired jimounocofficiency syndrome (AIDS), herpes viral infections and other viral infections) and proliferative mycocadial infections and other viral infections and other viral infections and toxin-induced liver diseases (such as that caused by stroken mycocadial infection and reperfusion injury), septic shock, cachaxia, morexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral arther and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and reperfusion injury), septic and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and coular diseases (such as alcohol). Twey are also useful in the preparation or recovery from surgery, trauma, radion therapy and transmiting mylogenesis and as adjuvants to enhance immune responstiveness
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                                                                              Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.
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Pred. No. 3.8e-137;
0; Mismatches 0;
   Albert VR,
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protein; 281

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AA031151

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RESULT 34 AAO31151

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The invention relates to an isolated antibody or its fragments such as VHCDR1 (heavy chain variable domain complementarity determining region), VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tumour necrosis factor; TNF-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or glioblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or a neurodegenerative disorder. The invention is useful in antibody therapy. The present sequence is human TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                       Human; protein coordinate data; heavy chain variable domain; VL; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; graft versus host disease; antibody therapy; nootropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody.
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                                                          TNF-related apoptosis-inducing ligand (TRAIL)
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Pred. No. 3.8e-137;
Mismatches 0;
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2002US-0384828P.
2002US-0396591P.
2002US-0403370P.
2002US-0425737P.
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llarity 100.0%;
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04-JUN-2002;
18-JUL-2002;
15-AUG-2002;
13-NOV-2002;
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FTVLLQSLCVAVTYVYFTNBLKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                     TRAIL Incyte 059509CD1
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Pred. No. 3.8e-137
Mismatches 0;
                                                                                                                                                                                                                                                           cancer; colon cancer
                                                                                                                                                                                                                                   Human TNF-related apoptosis inducing ligand
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Best Local Similarity 100.0%;
Matches 281; Conservative
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(JONE/) JONES D A.
(KARP/) KARPF A R.
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DNA methyla
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the Easidue position(s) selected from 20 positions such as S96C, S101C, S11C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C, S111C, V114C, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DR5.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, and further composition or an Apo-2 ligand variant polypeptide, and neuroprotective. The Apo-2 ligand variant polypeptide, inducing apoptosis in mammalian cells by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
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                                                                                                                            EYGLY
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                                                            LVIHEKG
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE:
                                                                                                                                                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Native human Apo-2 ligand protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein; 281
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N-PSDB; ADB61470.
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native; human
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the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or a immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the native human Apo-2 ligand protein the invention.
                                                                                                                                1 MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKOMQDKYSKSGIACFLKE
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N-PSDB; ADC35201.
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NARDELLI
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ne kinase; cytos
cancer; human.
                                          tumour necrosis factor family ligand. A composition comprising isolated antibody or its fragment is used for treating an indineed of decreased level of endokine alpha activity. The endokin polypeptide present in a heterotrimeric complex is used for traindividual having a disorder associated with excessive bone reserge osteoporosis, Paget's disease or arterial calcification. Individual having a disorder associated with insufficient bone comprises administering an endokine alpha antagonist, which is antibody that binds specifically to endokine alpha polypeptide present sequence represents the amino acid sequence of a tumoun
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                                    an isolated nucleic acid molecule
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protein tyrosine kinase pathway; protein tyrosine
gene therapy; drug sensitivity; genetic profile; c
                                                                                                                                                                                                                 Score 1478; DB 7;
Pred. No. 3.8e-137;
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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers, and cerrelating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynucleotides and (3) identifying polynucleotides and (2) identifying polynucleotides and (3) identifying polynucleotides and polypeptides, analysing the plurality of a microarray of polynucleotides or polypeptides, and selecting polynucleotides or polypeptides that predict the sensitivity or esistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides are useful in predicting the centivity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining drug sensitivity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining sensitivity of compounds that interact with protein tyrosine kinase pathways. These may be used in determining genetic profiles which aid in treating diseases and disorders (cancer) based on patient response at a molecular level. The present
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                   for predicting the activity of tyrosine kinases and/or protein
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          wew polynucleotides and polypeptides compounds that interact with protein tyrosine kinase pathways.
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This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumourigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.
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                                                              on injury
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antiarteriosclerotic; vulnerary; gene therapy; hypoxia-regulated condition; tumourigenesis; angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitric oxide synthesis; cancer; ischaemic condition; reperfusion injuration oxide synthesis; pre-eclampsia; atherosclerosis; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                    w substantially purified polypeptide, useful for diagnosing chypoxia-regulated condition, such as cancer, ischemia, reperitury, retinopathy, pre-eclampsia, atherosclerosis, inflammat
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                                                                                                                                                                                                                                                                                                                Mundy
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100.0%; Pred. No. 3.8e-137;
ive 0; Mismatches 0;
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05-OCT-2001;
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is human
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                                                                                                               TNF; DR3; T
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                                                                                                               disorder; tumour necrosis factor; TNF inflammatory bowel disease; Crohn's AlL; human.
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disorders of t
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95US-00461246.
98US-00005020.
98US-0074047P.
98US-00131237.
99US-0131963P.
99US-0132227P.
99US-0132227P.
99US-0132227P.
200US-0180908P.
200US-016879P.
200US-0216879P.
2001US-0216879P.
2001US-021809059.
2001US-0314381P.
2001US-0336695P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 necrosis factor of a disease or discrete bowel disease, Cr
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                     ABW02276 standard; protein;
                                                                                                               Gastrointestinal tract dise
TNF-gamma-beta protein; in:
ulcerative colitis; TRAIL;
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N-PSDB; AAD63912.
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TRAIL protein. 7
invention
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05-JUN-1995;
09-JAN-1998;
09-FEB-1998;
07-AUG-1999;
30-APR-1999;
03-MAY-1999;
03-MAY-1999;
03-MAY-1999;
03-MAY-1999;
03-MAY-1999;
04-TUL-2000;
27-APR-2000;
27-APR-2001;
06-JUL-2001;
24-AUG-2001;
07-DEC-2001;
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Score 1478; DB 7; Pred. No. 3.8e-137; Mismatches 0;

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Conservative

Local Similarity Les 281; Conser

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Query Match Best Local

100.0%;

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1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type of the invention is useful for a high-throughput method immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and cannot the composition is useful for detecting and to monitor the formulate prognosis and to design a treatment regimen and to monitor the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes;
LVIHEKG
                                                                                                                           FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                       FYY I YSQTYFRFQEEI KENTKNDKQMVQY I YKYTSYPDP I LLMKSARNSCWSKDAEYGLY
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FLSNLHLRNGE
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                                                                                                                                                                                                                                                                                                                                          standard; protein;
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N-PSDB; ADE76952.
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Gln at this location in the variant referred to in claim
17"
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claim 17"
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 acid
in a
                                                                                             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                             /note= "wild-type His may be substituted by Arg, Asp, Asn, Ala, Pro or Thr at this location in the variant referred to in claim 17"
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sequence represents the amino cDNA differentially expressed
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Xaa (where Xaa is encoded by an amber codon) at
location in the variant referred to in claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild-type Arg may be substituted by Lys location in the variant referred to in claim 17" 193
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location in the variant referred to in claim 17'
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Pred. No. 3.8e-137;
Mismatches 0;
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189
efficacy of treatment. The present sequence of a protein encoded by a liver disorder.
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                                                        Query Match
Best Local Similarity 100.0%;
Matches 281; Conservative (
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                                                                                                                                                                      The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence polypeptide, comprising 282 amino acids and having a sequence comprising 282 amino acids and having cone or more following amino acid substitutions at the residue positions or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant collypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence.

C current sequence that is referred to in claim 17 may contain cone or more of the potential substitutions highlighted in the features that is record.
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                                                                                                             useful for preparing a codisease, e.g., arthritis
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larity 100.0%; Pred. No. 3.8e-137;
Conservative 0; Mismatches 0;
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                                                                      Lindstrom SH;
                                                                                                          New Apo-2 ligand variant polypeptide, for treating cancer or immune-related multiple sclerosis.
                                                                                                                                                      Claim 17; SEQ ID NO 1; 111pp; English.
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                                                                     Kelley RF,
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                                                                                                                                                                                                                                                                                          'note= "wild-type Lys may be substituted for location in the variant referred to in claim
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Pred. No. 3.8e-137;
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1; Conservative
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Thr, Val or Lys at this location in the varian
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or Arg at this location in the variant referre
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                                                 yand variant polypeptide, useful for cancer or immune-related disease, e.
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immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence. Note: The variant sequence that is referred to in claim 2 may contain one or more of the potential substitutions highlighted in the features table
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       The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the wild-type human Apo-2 ligand amino acid
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in claim
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                                                                                                                                                                                                                                                                                                                   LVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "wild-type Gln may be substituted by Ly, this location in the variant referred to
                                                                                                                                                                                                                                                                                                                                                                        RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Apo-2 ligand with potential substitutions highlighted #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c; antiarthritic; neuroprotective; gene therapy; Apocancer; immune system disease; arthritis; multiple sc
                                                                                                                                                                                                                Length 281;
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                                                                                                                                                                                                                Score 1478; DB 8;
Pred. No. 3.8e-137;
Mismatches 0;
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189
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Best Local S
Matches 281
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The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence polypeptide, comprising 282 amino acids and having another polypeptide sequence comprising 282 amino acids and having cone or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents the human Apo-2 ligand amino acid sequence.

Note: The variant sequence that is referred to in claim 10 may contain one or more of the potential substitutions highlighted in the features table for this record.
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                                                                             , Glu,
referred
              /note= "wild-type Ile may be substituted by Leu, Met or
Val at this location in the variant referred to in claim
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g., arthritis or
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                                                                             /note= "wild-type Asp may be substituted by Ser,
Gln, Asp or Asn at this location in the variant
to in claim 10"
  claim 10"
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Pred. No. 3.8e-137;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   useful for disease, e.
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  referred
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  variant
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                                                                                                                                                                                                                                                                                                                   Lindstrom
location in the 266
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Best Local Similarity
Matches 281; Conser
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                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to apoptosis inducing molecule-I protein (AIM-I) comprising sequence that is 70 % identical to ADJ63976 or its mature for where the polypeptide binds antibody specific to AIM-I, induces apoptosic of cells. Also included are a composition comprising AIM-1 and a carrier, alm. I produced by a process involving expressing in a host cell a nucleic acid that encodes the protein so as to produce the protein (where the nucleic acid is chosen from a polynucleotide encoding AIM-1, mature AIM-1, mature/AIM-1 except for 1-5 or 5-10 conservative amino acid substitutions, the amino acid sequence encoded by human cDNA contained is ATCC Deposit No. 97448, and a polynucleotide that is complementary to polynucleotide which hybridises at 60degreesC in a hybridisation buffer consisting of 0.5 % SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl mature/AIM-1, and a polynucleotide chosen from polynucleotide encoding mature/AIM-1, and a polynucleotide encoding amino acid sequence encoded by human cDNA contained in ATCC Deposit No. 97448, where the polynucleotide encodes a polypeptide that has the same biological activity as described above). AIM-1 is useful for treating lyanged cell stimulating peripheral tolerance, destroying pathologic transformed cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at is complementary to
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and 0.1 % sodium dodecyl
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sequence encoded
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sis of T
ss and g
                                                                                                                                                                                                                                   Human; apoptosis inducing molecule 1; AIM-1; apoptosis; autoimmune disease; graft versus host disease; lymphadenopathy immunosuppressive; vasotropic; cytostatic; peripheral toleranc cell activation; cell proliferation; immune regulation; inflammatory response; systemic lupus erythematosus; imflammatory response; neoplasm; tumour; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel apoptosis inducing molecule polypeptide that induces apolecal line derived from pathological tissue and induces apoptosicells, useful for treating lymphadenopathy, autoimmune diseases versus host disease.
                   281
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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39. .281
/label= Mature AIM 1
'~~te= "Claimed in claim 1"
                                                                                                                                                                                                      AIM-1
                                                                                                                                                                                                                                                                                                                                                                                                                        "Signal peptide"
                                                                                                                                                                                                      Human apoptosis inducing molecule 1,
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                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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97US-00816981
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N-PSDB; ADJ63975.
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13-MAR-1997;
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lines, mediating cell activation and proliferation. AIM-1 proteins are functionally linked as primary mediators of immune regulation and inflammatory response, are useful for diagnosis and treatment of disorders of cells, tissues and organisms. AIM-1 is useful as research tool in elucidating biology of autoimmune disorders including systemic lupus erythematosus, immunoproliferative disease lymphadenopathy and is useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also useful to treat diseases which required growth promotion activity e.g., restenosis. AIM-1 is useful for assessing AIM-I binding capacity of its binding molecules such as receptor molecules. The present sequence
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disease;
gene therapy; human.
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                                                                                                                                                                                 Score 1478; DB 8;
Pred. No. 3.8e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis inducing molecule-I; AIM-I; cell a cell differentiation; apoptosis; autoimmune graft-versus-host disease; lymphadenopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human apoptosis inducing molecule-I
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                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 281; Conservative
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N-PSDB; ADL71815.
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13-MAR-1997;
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                                             The invention relates to antibodies specific to apoptosis inducing molecule-I (AIM-I) polypeptides. The invention is useful in research, biological, diagnostic, clinical or therapeutic applications. It is also used for modulating activation and differentiation of cells, both normally and in disease states, or for mediating apoptosis and preventing or treating autoimmune diseases, graft-versus-host disease or lymphadenopathy. The invention is also useful in gene therapy. The present sequence is human AIM-I protein.
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                                                                                                                                                         Score 1478; DB 8;
Pred. No. 3.8e-137;
Mismatches 0;
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The invention relates to a new purified tumour necrosis factor related apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid sequence that is at least 90% identical to human TRAIL (ADK15498) or mouse TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat cells. Also included are a purified human TRAIL polypeptide encoded by the cDNA insert of the recombinant vector deposited in strain ATCC 69849 or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces apoptosis of Jurkat cells), a fusion protein comprising a leucine zipper opptide and a soluble TRAIL polypeptide (comprising the extracellular comprising at least two soluble TRAIL polypeptides (or at least two soluble TRAIL polypeptide is useful in studies of an oligomer defined above). The TRAIL polypeptide is useful in studies of apoptosis, in regulating programmed cell death, for treating leukaemia, cancer (e.g. colorectal cancer) or viral infections, or in purifying cancer (e.g. colorectal cancer) or viral infections, or in purifying cucance development. The TRAIL polypeptide may also be used in developing treatments for any disorder mediated by defective or insufficient amounts of TRAIL. The present sequence represents human TRAIT.
                                                                                                                                                                                                                                                                           New tumor necrosis factor related apoptosis inducing ligand polypeptides useful in studies of apoptosis, in regulating programmed cell death, or for treating leukemia, cancer (e.g. colorectal cancer) or viral
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Pred. No. 3.8e-137;
Mismatches 0;
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            95US-00496632.
95US-00548368.
96US-00670354.
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99US-00320424.
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|| Similarity 100.0%;
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N-PSDB; ADK15497.
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01-NOV-1995;
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10-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to apoptosis inducing molecule I (AIM-I) polypeptide and the encoding polynucleotide useful in biological, diagnostic, clinical and therapeutic arts. The invention is useful in treating autoimmune disorders such as systemic lupus erythematosus, immunoproliferative disease lymphadenopathy (IPL), angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis, diabetes and multiple sclerosis, graft versus host disease, lymphoproliferative disease such as lymphadenopathy, in inhibiting neoplasia such as tumour cell growth, in treating restenosis and regulating haematopoiesis in endothelial cell development. The invention is useful in chromosome identification and as a diagnostic marker for determining expression of AIM-I polypeptide in tumour cell lymphoma. The including pancreatic tumour, endometrial tumour and T-cell lymphoma.
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                                                                                                                                Apoptosis inducing molecule I; AIM-I; therapeutic; autoimmune
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Pred. No. 3.8e-137;
Mismatches 0;
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              281 AA
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97US-00816981
              ADN07587 standard; protein;
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13-MAR-1997;
                                                                       17-JUN-2004
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WF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; maniarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; mmunosuppressive; vulnerary; gene therapy; immune disorder; immunosuppressive; vulnerary; gene therapy; immune disorder; hodgkin's lymphoma; haematopoietic tumour; whepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; whyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; Writal infection; HIV-1; HILV-1; hepatitis B; hepatitis C; BBV; influenza; wiral infection; host cell survival; evasion of immune response; wherematoid arthritis; inflammatory bowel disease; colitis; asthma; anteomatoid arthritis; inflammatory bowel disease; colitis; asthma; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; mecrotic lesion; wound; organ transplant rejection; ancer; while we have the propagation; human.
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disorders or
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                         FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotides and polypeptides associated pathway, useful for diagnosing, treating, or preventing diseases associated with NF-kappaB pathway.
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2003US-0469757P
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                                                                                                                                                                                                                                                 standard; protein;
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N-PSDB; ADR14208.
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12-MAY-2003;
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or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder, cancer, aberrant apoptosis, related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTIV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human protein which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but
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281 AA; Sequence

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                                               MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSG
                                                             MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSG
                                                                                            DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL)
                                                                                                              DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL
                                                                                                                                          RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
Length 281;
                        Indels
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Score 1478; DB 8;
Pred. No. 3.8e-137;
Mismatches 0;
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281; Conser
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Matches 281
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antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor; haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma; chronic myelogenous lymphoma; multiple myeloma; chronic lymphocytic leukaemia; scFv; human; TRAIL; TNF-related apoptosis-inducing ligand. amino acid sequence SEQ ID NO:66 standard; protein; (first entry) Human TRAIL 18-NOV-2004 ADK82215; ADK82215 ADK82

2003WO-US025457 WO2004016753-A2 15-AUG-2003; sapiens Ношо

2002US-0403382P 2002US-0425730P

15-AUG-2002; 13-NOV-2002;

tumour inhibition; tumour treatment; metastasis; infectious lesion; antigen presenting cell; immunostimulatory cytokine; cytostatic; vulnerary; immunomodulator; melanoma; hepatoma; adenocarcinoma;

Tumour treatment-related human protein sequence SeqID36

entry)

(first

18-NOV-2004

ADS88000;

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281

ADS88000 standard; protein;

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The present invention describes an antibody or its fragment comprising a VH and VL domain that is at least 80% identical to a VH and a VL domain that is at least 80% identical to a VH and a VL domain of an antibody expressed by any one of the cell lines contained in American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-3570 and PTA-3675, where the antibody specifically binds TR4 (TRAIL receptor). Also described is a pharmaceutical composition for treating or preventing haematological cancer, comprising the antibody or its fragment and a member selected from ibritumomab tiuxetan, imatinib mesylate, cortostatic activity, and can be used in immunotherapy. The antibody or its fragment can be used for the preparation of a pharmaceutical composition for treating or preventing haematological cancer, e.g. Nonthodykin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or chronic lymphocytic leukaemia. The present sequence represents human tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL), which is used in the exemplification of the present invention.
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                                                                                                                       Use of an antibody or its fragment the specifically binds to TR4, for preparation of a pharmaceutical composition for treating or preventing hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or
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                                                           Albert
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                                                             Rosen
06-MAY-2003; 2003US-0468050P
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                                                             Ruben SM,
                              (HUMA-) HUMAN GENOME
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This invention relates to a novel method of inhibiting or treating a tumour, metastasis or infectious lesion in a subject which comprises administering into or near a site of a tumour or infectious lesion in a subject an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine. The invention may be useful for the production of compounds with a cytostatic or vulnerary activity acting as immunomodulators. The method is useful in inhibiting or treating a tumour, metastasis or infectious lesion in a subject, where the size of tumour, metastasis (where number is also decreased) or infectious the tumour, metastasis (where number is also decreased) or infectious concerinoma, colorectal cancer, basal cell cancer, oral cancer, nead and neck cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostrate cancer, testicular cancer and breast cancer. The present sequence is that
                                                                                                                                                                                                                                                                                                                                                                                                                                    n comprises
      eal cancer;
                                            cancer;
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                                                             cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   or treating a tumor, metastasis or infectious lesion ing into or near site of a tumor or infectious lesion senting cell and an immunostimulatory cytokine or a ring the cytokine.
colorectal cancer; basal cell cancer; oral cancer; nasopharyng laryngeal cancer; bladder cancer; head cancer; neck cancer; renal cell cancer; pancreatic cancer; pulmonary cancer; cervicovarian cancer; oesophageal cancer; gastric cancer; prostrate testicular cancer; breast cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 36; 169pp; English
                                                                                                                                                                                                                              2003WO-US032827
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N-PSDB; ADS87999.
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testicular canc
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                                                                                                                Homo sapiens.
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ö 180 120 180 240 240 9 9 HILLI DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ Gaps ö Length 281; Indels SIYOGGI FELKENDRI FVSVTNEHLI DMDHEASFFGAFLVG SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG Score 1478; DB 8; Pred. No. 3.8e-137 Mismatches 0; ·, 100.0%; Similarity 100 11; Conservative Sequence 281 AA; Query Match Best Local Sim: Matches 281; Н 61 121 241 121 181 181 241

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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancersesociated proteins. Also included are an expression vector comprising the above recombinant nucleic acid crexpression vector, a microarray for detecting a cancer-associated caid cited above, a host cell comprising the above a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a A sequence selected from any of the 35 polynucleotide sequences as mentioned in the specification, or its opportunity in isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical excipient, a kit for detecting cancer cells comprising the above monoclonal antibody, a pharmaceutical excipient, a kit for detecting cancer cells in an individual, an electronic library comprising the above polypeptide (or their fragments), methods for diagnosing cancer cells in an individual, an electronic library comprising the above polymetotide or polypeptide (or their fragments), methods of sortening for anticancer activity or for a bloactive agent capable of modulating the associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of a sectivity or a carrivity or for a bloactive agent capable of modulating chargement associated with expression of a polypeptide in a test cell sample. CA gene in a call with a method for treating cancers and a method for inhibiting cancer. The present sequence is a human CAP cancer. The present sequence is a human CAP cancer of the printed sequence data for this patent din or form pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
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for diagnosing, preventing or treating cancers, especially lymphoma
leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                  cancer-associated protein; cytostatic; cancer; leukaemia;
                                                                                                                                            Human cancer-associated protein HP7-053.3
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                     standard; protein; 281 AA
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2003US-00388838.
2003US-00417375.
2003US-00461862.
2003US-00663431.
2003US-00737318.
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                                                                                                    (first entry)
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14-MAR-2003;
15-APR-2003;
13-JUN-2003;
15-SEP-2003;
15-DEC-2003;
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                                                                                                                                                                                                         lymphoma;
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                                                            AB084415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
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les 281; Conservative
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N-PSDB; ADP23387.
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                      281
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of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, invenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease mellitus, immune-mediated renal disease, a demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, bilary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitis, enteropathy, whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermatitis, poortasis, of the lung, cosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.
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version
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(c) 1993
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1 MAMMEVQGGPSLGQTCVLIV US-10-662-431-2 1478 **Bcore** Sequence: Perfect

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281

1465611 hits satisfying chosen parameters: residues 1465611 segs, 345679903 of Total number

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2000000000 length: length: seq sed DB DB Minimum Maximum

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Applicati Published Database

Published Applications AA:*

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(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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SUMMARIES

Sequence 8 Sequence 1 Sequence 8 Sequence 1 Sequence 5 Sequence Descript US-08-916-625B-6 US-08-971-317A-8 US-09-193-663-8 US-09-934-465-1 US-09-919-039-118 US-09-919-039-118 US-10-011-125-4 US-10-001-054-54 US-10-093-766-54 US-10-151-882-41 US-10-322-673-72 DB 281 281 281 281 281 281 281 281 281 Length Query Match 11478 11478 114478 114478 11478 11478 Score Result No. 1264897611119991919

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US-10-139-785-66		US-10-279-68	US-10-29	US-10-333-712-	US-10-662-42	US-10-202-062-	US-10-662-43	US-10-662-430-	US-10-652-244-	US-10-381-160-	US-10-755-889-	US-10-491-32	US-10-771-254-	US-10-855-559-	US-10-451-20	US-10-495-353-	US-10-652-979-	US-10-066-209-	US-10-367-094-2	US-10-978-2	-855-544A-1	-09-855-544A-1	US-10-652-244-1	US-10-652-244-1	Þ	US-10-38	US-10-389-22		09-855-5	>	US-10-017-91
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ALIGNMENTS

Sequence 6, Application US/08916625B

Publication No. US20010010924A1

GENERAL INFORMATION:

APPLICANT: DEEN, KEITH C.

APPLICANT: YOUNG, PETER R.

TITLE OF INVENTION: RECEPTOR, TR6

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,625B
FILING DATE: 22-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
FILING DATE: 14-MARCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION: 19482 US-08-916-625B-6 RESULT

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Pred. No. 1.3e-128;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 1L
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08971317A Publication No. US20010010925A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
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TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acids
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                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Pred. No. 1.3e-128;
Mismatches 0;
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Pred. No. 1.3
0; Mismatches
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Sequence 17, Application US/09813329

Patent No. US20020012968A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20020012968A1el Dr.

TITLE OF INVENTION: Variants Thereof

FILE REFERENCE: D0016.np

CURRENT APPLICATION NUMBER: US/09/813,329

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.0
                                                         No. US20010010925Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Drosophila melanogaster US-09-813-329-17
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Local Similarity 100.0%;
nes 281; Conservative 0;
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Best Local Similarity 100.0%;
Matches 281; Conservative
                  LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US200100
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  N FOR SEQ ID NO:
CHARACTERISTICS
INFORMATION F
SEQUENCE CH
LENGTH:
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US-08-971-317A-8
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LENGTH: 281
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Pred. No. 1.3e-128;
0; Mismatches 0;
  1.3e-128;
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OTHER INFORMATION: Incyte ID No. US20030108871A1-09-919-039-118
 red. No. 1. Mismatches
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; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREA;
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
  Pred.
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llarity 100.0%;
Conservative
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ORGANISM: Homo sapiens
 Local Similarity
hes 281; Conser
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Best Local S
Matches 281
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TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THE
FILE REFERENCE: 6255.US.02

CURRENT APPLICATION NUMBER: US/09/193,663

CURRENT FILING DATE: 1998-11-17

EARLIER APPLICATION NUMBER: 60/065,916

EARLIER FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.3
0; Mismatches
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TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
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US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
                                                                                                            US/09193663
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Best Local Similarity 100.0%;
Matches 281; Conservative (
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                                                                                                          Sequence 8, Application US Patent No. US20020055624A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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R APPLICATION NUMBER: 09/403297
R FILING DATE: 1999-10-18
R APPLICATION NUMBER: 09/423741
R FILING DATE: 1999-11-10
R APPLICATION NUMBER: 09/709238
R FILING DATE: 2000-11-08
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-12
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-01
R APPLICATION NUMBER: 60/05
R APPLICATION NUMBER: 60/05
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/05
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R FILING DATE: 1998-11-19
R APPLICATION NUMBER: 09/21
R FILING DATE: 1998-12-22
R APPLICATION NUMBER: 09/26
PRIOR 
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Pred. No. 1.3e-128;
Mismatches 0;
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APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Hebert, Carolyn
APPLICANT: Hebert, Carolyn
APPLICANT: Hebert, Carolyn
APPLICANT: Kabakoff, Rhona
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034RIPCT
CURRENT APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-34
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083545
                                                                                                                STRAINS
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
                 Sequence 4, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST
FILE REFERENCE: P1804R1
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US-10-011-125-4
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281; Conser
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## APPLICATION NUMBER: 60/100293
| FILING DATE: 1998-09-15
| APPLICATION NUMBER: 60/101476
| RAPPLICATION NUMBER: 60/101476
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| RAPPLICATION NUMBER: 60/107783
| RAPPLICATION NUMBER: 60/102423
| RAPPLICATION NUMBER: 60/10249
| RELING DATE: 1998-11-18
| RAPPLICATION NUMBER: 60/112420
| RAPPLICATION NUMBER: 60/11554
| RAPPLICATION NUMBER: 60/11554
| RAPPLICATION NUMBER: 60/115554
| RAPPLICATION NUMBER: 60/115558
| RAPPLICATION NUMBER: 60/115558
| RAPPLICATION NUMBER: 60/11558
| RAPPLICATION NUMBER: 60/11558
| RAPPLICATION NUMBER: 60/131294
| RELING DATE: 1999-01-20
| RAPPLICATION NUMBER: 60/141037
| RAPPLICATION NUMBER: 60/141037
| RAPPLICATION NUMBER: 60/141037
| RAPPLICATION NUMBER: 60/141037
| RAPPLICATION NUMBER: 60/144758
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OR APPLICATION NUMBER: 09/380137

OR PILING DATE: 1999-08-25

OR APPLICATION NUMBER: 09/380138

OR APPLICATION NUMBER: 09/380138

OR RILING DATE: 1999-08-25

OR RELING DATE: 1999-08-25

OR RELING DATE: 1999-08-25

OR RELING DATE: 1999-08-25
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60/087607
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R APPLICATION NUMBER: 60/05
R FILING DATE: 1998-08-17
R APPLICATION NUMBER: 60/05
R FILING DATE: 1998-09-10
R APPLICATION NUMBER: 60/10
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A PAPLICATION NUMBER: 09/8182636

BR APPLICATION NUMBER: 09/924419

BR FILING DATE: 2001-08-18

BR FILING DATE: 1999-09-04

BR FILING DATE: 1999-01-06

BR APPLICATION NUMBER: PCT/US99/0815

BR FILING DATE: 1999-01-08

BR PELING DATE: 1999-01-08

BR PELING DATE: 1999-01-08

BR PELING DATE: 1999-01-08

BR FILING DATE: 1999-01-08

BR PELING DATE: 1999-01-01

BR PELING DATE: 1999-12-01

BR PELING DATE: 2000-02-18

BR PELING DATE: 2000-03-15

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APPLICATION NUMBER: PCT/US00/32678
    09/802706
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NUMBER: 09/
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NUMBER: 09/
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FILING DATE: 2001-0
APPLICATION NUMBER:
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i Sequence 54, Application US/10093766

j Publication No. US20030013099A1

j GENERAL INFORMATION:

j APPLICANT: Lasek, Amy W.

j APPLICANT: Karpf, Adam R.

j TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS

j FILE REFERENCE: PA-0047 US

j CURRENT APPLICATION NUMBER: US/10/093,766

j CURRENT FILING DATE: 2002-03-07

j NUMBER OF SEQ ID NOS: 61

s SOFTWARE: PERL PROGram

j SEQ ID NO 54

j LENGTH: 281
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CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: Incyte ID No. US20030013099A1
US-10-093-766-54
                                                                                                                                                                                                                                                                                                                                                                            Score 1478;
Pred. No. 1.3
; Mismatches
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
TYPE: PRT
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Query Match

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Sequence 20, Application US/10218547
Sequence 20, Application US/10218547
Publication No. US20030100074A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases
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Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
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Pred. No. 1.3e-128
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 281; Conservative
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ORGANISM: Homo sapiens
-10-151-882-41
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SNGTH: 281
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                                     CVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSG
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MEDIUM TYPE: 3.5 Diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pharmacia & Upjohn, Intellectual
Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
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 Pred. No. 1.3e-128;
Mismatches 0;
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FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related DE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         b
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REGISTRATION NUMBER: 41,11
REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10174654
Publication No. US20030044937A1
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michae
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TYPE: amino acid
Similarity 100.0%; P
11; Conservative 0;
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INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS
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| Sequence 66, Application US/10139785
| Publication No. US20030190685A1
| GENERAL INFORMATION:
| APPLICANT: Salcedo et al.
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TITLE OF INVENTION: Receptors
| TITLE OF INVENTION: Receptors
| TITLE OF INVENTION: Receptors
| FILE REFERENCE: PF550
| CURRENT APPLICATION NUMBER: US/10/139, 785
| CURRENT FILING DATE: 2002-04-05
| PRIOR FILING DATE: 2001-12-20
| PRIOR FILING DATE: 2001-11-14
| PRIOR FILING DATE: 2001-11-07
| PRIOR FILING DATE: 2001-11-07
| PRIOR FILING DATE: 2001-10-09
| PRIOR FILING DATE: 2001-10-09
| PRIOR FILING DATE: 2001-10-09
| PRIOR FILING DATE: 2001-09-21
| PRIOR APPLICATION NUMBER: 60/323,807
| PRIOR FILING DATE: 2001-09-21
| PRIOR APPLICATION NUMBER: 60/309,176
| PRIOR FILING DATE: 2001-08-02
| PRIOR FILING DATE: 2001-08-02
| PRIOR FILING DATE: 2001-08-02
| PRIOR FILING DATE: 2001-06-04
| PRIOR PRILING DATE: 2001-06-04
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Pred. No. 1.3e-128;
Mismatches 0;
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Sequence 72, Application US/10322673

Publication No. US20030180296A1

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TITLE OF INVENTION: Receptors

FILE REFERENCE: PF585

CURRENT APPLICATION NUMBER: US/10/322,673

CURRENT FILING DATE: 2002-12-19

PRIOR PILING DATE: 2001-12-20

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-01-13

PRIOR FILING DATE: 2002-11-13
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Pred. No. 1.3e-128;
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Pred. No. 1.3e-128;
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                                                                                                                                                                                                                                                                                   Mismatches
     Human Endokine Alpha
TITLE OF INVENTION: Human Endokine Alphe
FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
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nes 281; Conservative
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Best Local Similarity
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CRGANISM: human
US-10-218-547-20
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ENGTH: 281
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0-322-673-7
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Best Local S
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Sequence 5, Application US/10292486

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies That Immunospecifically Bind To

FILE REFERENCE: PF532P1

CURRENT APPLICATION NUMBER: US/10/292,486

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: 60/403,376

PRIOR FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/377,973

PRIOR FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/331,309
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Pred. No. 1.3e-128;
Mismatches 0;
                                                                                                                                Sequence 8, Application US/10279687
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THI
; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR FILING DATE: 1998-11-17
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
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llarity 100.0%;
Conservative
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281; Conser
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US-10-279-687-8
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                                       APPLICANT: Wei, Ping
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory
TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
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                                                                                             Score 1478; DB 14;
Pred. No. 1.3e-128;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/310,793

CURRENT APPLICATION NUMBER: US/10/310,793

CURRENT FILING DATE: 2002-12-06

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1999-05-03

Remaining Prior Application data removed - S

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 26

LENGTH: 281

TUBGETH: 281
                                                                                                                                                             RESULT 15
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
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ilarity 100.0%; P
Conservative 0;
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APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig
APPLICANT: Zhang, Jun
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281; Conser
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US-10-310-793-26
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               MAMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/662,429
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               281
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[.3e-128;
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FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                              Inducing
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Pred. No. 1
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SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis II
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome SC:
STREET: 9410 Key West Aveni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1) 309-8504
309-8512
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Publication No. US20040038347A1
GENERAL INFORMATION:
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larity 100.0%;
Conservative (
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 281; Conser
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Publication No. US20040005314A1

GENERAL INFORMATION:
APPLICANT: Escandon, Enrique
APPLICANT: Fox, Judith A.
APPLICANT: Kelley, Sean K.
APPLICANT: Xiang, Hong
TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
FILE REFERENCE: P1838R1
CURRENT APPLICATION NUMBER: US/10/333,712
CURRENT FILING DATE: 2003-01-23
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 4
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Pred. No. 1.3e-128;
Mismatches 0;
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Pred. No. 1.3
; Mismatches
      PRIOR APPLICATION NUMBER: 09/986,149
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,359
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 47
    NUMBER: 09/986,149
2001-11-07
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2001-11-14
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                                                                                                                                                                                               ; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5
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ORGANISM: Homo Sapien
-10-333-712-1
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Matches 281; Conser
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US-10-333-712-1
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Best Local S
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ZIP: 400-COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/062,431
FILING DATE: 16-Sep-2003
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
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Pred. No. 1.3e-128;
Mismatches 0;
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; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Apoptosis Inducing Mo
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, In
STREET: 9410 Key West Avenue
; STATE: MD
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TYPE: amino acid
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larity 100.0%;
Conservative (
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
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ZIP: 20850
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MEDIUM TYPE: F
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US-10-662-430-2
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TITLE OF INVENTION: Heteromultimeric TNF Ligand Family
FILE REFERENCE: PF559
CURRENT APPLICATION NUMBER: US/10/202,062
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
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Pred. No. 1.3e-128;
Mismatches 0;
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TITLE OF INVENTION: Apoptosis Inducing
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
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US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
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US-10-652-244-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICANT: Wiley, Steven R.

APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION: Cytokine that Induces Apoptosis

FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/10/652,244

CURRENT FILING DATE: 2003-09-02

PRIOR FILING DATE: 2001-02-27

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1999-05-26

PRIOR FILING DATE: 1998-11-10

PRIOR FILING DATE: 1998-11-10

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1996-06-25

PRIOR APPLICATION NUMBER: 08/670,354

PRIOR FILING DATE: 1996-06-25
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                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/662,430
FILING DATE: 16-Sep-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                   APPLICATION NUMBER: US/08/816,981
FILING DATE: 13-MAR-1997
                                                                                                                                                             NAME: Kimball, Paul, C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PF261
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                     LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-662-430-2
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                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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TELEFAX: (301) 309-
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
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US-10-652-244-2
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DB 16;

Score 1478; Pred. No. 1

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RESULT 24
US-10-381-160-5
; Sequence 5, Application US/10381160
; Publication No. US20040131587A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
; FILE REFERENCE: 2993-WO
; CURRENT APPLICATION NUMBER: US/10/381,160
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/242,868
; NUMBER OF SEQ ID NOS: 6
; SOUTH FOR SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT

TYPE: PRT
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Pred. No. 1.3e-128
; Mismatches 0;
                   496,63
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PRIOR FILING DATE: 1995-11-01
PRIOR APPLICATION NUMBER: 08/49
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 281
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    Homo
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Matches 281;
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                                                                                                                 Sequence 210, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKS
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; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Robert F. Kelley, Stephanie H. Lindstrom
; TITLE OF INVENTION: AP0-2 Ligand Variants and Uses Thereof
; FILE REFERENCE: P1858R1
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 6
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Pred. No. 1.3e-128;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/755,889

CURRENT FILING DATE: 2004-01-13

PRIOR APPLICATION NUMBER: U.S. 60/440,068

PRIOR FILING DATE: 2003-01-14

PRIOR APPLICATION NUMBER: U.S. 60/469,757

PRIOR FILING DATE: 2003-05-12

NUMBER OF SEQ ID NOS: 823

SOFTWARE: Patentin version 3.2

LENGTH: 281
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Best Local Similarity
Matches 281; Conser
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US-10-755-889-210
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US-10-491-326-1
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Patin Docket Preview

APPLICANT: Lin, Tanya P.

APPLICANT: Lin, Tanya P.

APPLICANT: Shahrokh, Zahra

APPLICANT: Shahrokh, Zahra

APPLICANT: Matthews, Timothy C.

TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS

FILE REFERENCE: P1857R1P1

CURRENT APPLICATION NUMBER: US/10/771,254

CURRENT FILING DATE: 2004-02-03

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
Score 1478; DB 16;
Pred. No. 1.3e-128;
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Pred. No. 1.3e-128;
Mismatches 0;
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                       Mismatches
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US-10-771-254-1
; Sequence 1, Application US/10771254
; Publication No. US20050020498A1
; GENERAL INFORMATION:
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APPLICANT: FLORES, Heather
APPLICANT: DAI, Roger
APPLICANT: PAI, Roger
APPLICANT: PAI, Roger
APPLICANT: MATTHEWS, Timothy
TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
FILE REFERENCE: P1857R1
CURRENT APPLICATION NUMBER: US/10/495,353
CURRENT FILING DATE: 2004-05-12
PRIOR PILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
CORGANISM: Homo sapiens
US-10-495-353-1
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Mismatches 0;
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Pred. No. 1.3e-128;
0; Mismatches 0;
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Publication No. US20050080006A1
GENERAL INFORMATION:
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Similarity 100.0%;
281; Conservative 0
                               Similarity 100.0%; Similarity 100.0%; 31; Conservative
; ORGANISM: Homo sapiens
US-10-451-200-5
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Subjication No. US20050048645A1
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: METHOD OF TREATING OR PREVENTING DISEASE CHARACTERIZED BY
TITLE OF INVENTION: NEOFORMANS INFECTION
FILE REFERENCE: 2966-WO
CURRENT APPLICATION NUMBER: US/10/451,200
CURRENT FILING DATE: 2003-06-21
PRIOR FILING DATE: 2001-01-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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or Proapoptotic (
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        241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                 Sequence 2, Application US/1085559

Publication No. US20050031593A1

GENERAL INFORMATION:

APPLICANT: Harding, Thomas

APPLICANT: Lalani, Alshad

APPLICANT: Lalani, Alshad

APPLICANT: Donahue, Brian

TITLE OF INVENTION: Method for Treating Cancer By Ver

TITLE OF INVENTION: One or More Anti-Angiogenic or FILE REFERENCE: 3802-094-27

CURRENT APPLICATION NUMBER: US/10/855,559

CURRENT FILING DATE: 2004-05-28

PRIOR APPLICATION NUMBER: US 60/475,006

PRIOR FILING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.3e-128;
0; Mismatches 0;
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0
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                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapien
US-10-855-559-2
                                                                                                                                                                                                                                                                               LENGTH: 281
TYPE: PRT
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Best Local S
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SEQ ID NO 5
LENGTH: 2
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Pred. No. 8.5e-128;
); Mismatches 0;
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Pred. No. 1.4e-126;
0; Mismatches 0;
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; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Target
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                          Version
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100.0%; P.
               057
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/05
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 3
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Best Local Similarity 99.3%;
Matches 279; Conservative
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                                                                                                               ; ORGANISM: HOMO SAPIENS
US-10-066-209-3
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US-10-367-094-22
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Best Local Similarity
Matches 279; Conser
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US-10-367-094-22
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LENGTH: 279
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; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTOR
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT APPLICATION NUMBER: 09/072,993
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1998-05-06
; PRIOR FILING DATE: 1997-08-13
; PRIOR FILING DATE: 1997-08-13
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Pred. No. 1.3e-128;
Mismatches 0;
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/652,979
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 09/060,533
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
                                                                                                Sequence 1, Application US/10652979; Publication No. US20050089958A1; GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Schwall, Ralph H.
TITLE OF INVENTION: Apo-2 Ligand; FILE REFERENCE: P0978P3C1
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FNGTH: 281
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US-10-652-979-1
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US-10-066-209-3
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US-10-978-203-23
i Sequence 23, Application US/10978203
j Publication No. US20050112666A1
i GENERAL INFORMATION:
i APPLICANT: Chicheportiche, Yves
i APPLICANT: Chicheportiche, Yves
i APPLICANT: Chicheportiche, Yves
i TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
i FILE REFERENCE: A003
i CURRENT FILING DATE: 2004-10-29
i FRIOR APPLICATION NUMBER: 60/023,541
i PRIOR FILING DATE: 1996-08-07
i PRIOR FILING DATE: 1996-10-18
i PRIOR FILING DATE: 1996-10-18
i PRIOR FILING DATE: 1997-03-18
i NUMBER OF SEQ ID NOS: 27
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO 23
i LENGTH: 283
i TYPE: PRT
i ORGANISM: homo sapien
US-10-978-203-23
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                          SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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Pred. No. 8.1e-125;
); Mismatches 1;
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Best Local Similarity 97.5%;
Matches 278; Conservative
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- protein search, using sw model OM protein

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281 US-10-662-431-2_COPY_39_ 1287 score:

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

512079187 residues 1612378 seqs, Searched:

804456 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_grot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	z5 brack	39	marmo	canie	homo	homo	macac	Oggyh9 mus musculu		_		Q8aw02 cyprinus ca		Q6t9c7 brachydanio	P04924 oryctolagus	Q91z14 sigmodon hi	Q9bee8 erinaceus e	per		cavia por	pagrue	sus scrof	P36939 peromyscus	jg37	6600 bos taurus	ib42 para	9553	9nd1	34 ma	Q9bec4 talpa europ	
SUMMARIES	H	Q9DDZ5	Q6JSD9	Q9WV90	967306	TN15 HUMAN	TN14 HUMAN	Q8MJ <u>1</u> 9	TN14 MOUSE	Q7T2 <u>Q</u> 3	070332	Q6U817	QBAW02	Q80XA4	Q6T9C7	TNFA RABIT	Q91Z <u>L</u> 4	Q9BEE8	Q9ERG6	TNFB PIG	TNFA_CAVPO	Q7T1 <u>U</u> 4	TNFA_PIG	TNFA_PERLE	Q8JG37	TNFB BOVIN	Q9IB <u>4</u> 2	TNFA HORSE	Q99N <u>D</u> 1	TNFA MARMO	Q9BEC4	
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RESULT Q6JSD9

P01375 homo sapien Q6x658 marmota mon P51743 cervus elap P01374 homo sapien P61125 pan troglod Q8hzd9 pan troglod Q9ib41 paralichthy P06804 mus musculu P16599 rattus norv Q9jm09 marmota mon P33620 papio sp. (Q8awc9 cyprinus ca Q80we7 peromyscus	AA. e update) ion update) io). Vertebrata; Euteleostomi; Ostariophysi; Cypriniformes; NF receptor and two TNF 129:475-481(2001).	EA. Bis factor receptor binding; IEA. Onse; IEA. 1y. Score 305.5; DB 2; Length 214; Pred. No. 4.4e-17; Mismatches 59; Indels 7; Gaps 3; LESSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 136 LESSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 136 DMHQPQFDLHQSCRHPVHTW-ANKSFGAHLYNMTLTNGRL 105
1 TNFA HUMAN 2 Q6X658 1 TNFA CEREL 1 TNFB PANTR 1 TNFB PANTR 2 Q91841 1 TNFA PANTR 1 TNFA RAT 1 TNFA RAT 1 TNFA RAT 1 TNFA RAT 2 Q8AWC9 2 Q8AWC9 2 Q8AWC9 1 TNFA TURTR	PRT; 214 AA.6, Created) 6, Last sequence us; Last annotation 15, Last annotation 15, Last annotation 11; Teleostei; Ost	i i i i i i i i i i i i i i i i i i i
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	PRELIMINARY (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. I) retio (Zebretazoa; Choii, Neopter Choii, Neop	-GENE-010801-1; tn 16020; C:membrane; 05164; F:tumor nec 06955; P:immune rei 1PR008983; TNF_1i 1PR008983; TNF_1i 1PR008983; TNF_1i 1PR008983; TNF_1i 1PR008983; TNF_1i 0229; TNF; 1. D002012; TNF; 1. 223.7%; imilarity 37.6%; imilarity 37.6%; conservative
32 123 34 122.5 35 122 36 122 37 122 39 121.5 39 121 40 121 42 120 43 120 44 119		WELLN; ZDB-GER GO; GO:00160 GO; GO:00069 InterPro; IP InterPro; IP ProDom; PD0022 PROSITE; PSS SEQUENCE 2 SEQUENCE 2 Ouery Match Best Local Simi Matches 62;
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169 AA;
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Best Local S
Matches 42
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                    Query Match
Best Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae
                                                                                      Euteleostomi
                                                                                                                                                                                                                                                                                       52
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GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0016020; C: membrane; IEA.
GO; GO: 00069164; F: tumor necrosis factor receptor binding; IEA.
GO; GO: 0006915; P: apoptosis; IEA.
GO; GO: 0007165; P: immune response; IEA.
GO; GO: 0007165; P: signal transduction; IEA.
InterPro; IPR008064; Fas ligand.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF subf.
                                                                                                                                                     Lahesmaa
                                                                                                                                                                                                                                                                             THELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWOLROLVRK
                                                                                                                                                                                                                                                                    TNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK
                                                                                                                                                                                                                             63;
                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chemokine tumor necrosis factor ligand superfamily member
                                                                                               Ношо
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                                                                                                                                                West A., Saarikko I
1 T., Mannila H., La
                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                             Length
                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                         8F0C7936DA5AA6E6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                            Score 291; DB 2;
Pred. No. 1.4e-16;
 63 AA
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                Polvi A., Ruosaari S., Vendelin J., West
Reinikainen A., Hollmen J., Laitinen T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hodgson P.D., Grant M.D., Michalak T.I., "Perforin and Fas/Fas ligand-mediated cychronic woodchuck viral hepatitis."; Clin. Exp. Immunol. 118:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                          Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Healthy liver;
MEDLINE=20010026; PubMed=10540161
                                                                                                                                                                                                                                             0;
                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                            22.6%;
100.0%;
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                                                                                                                                                                                                        7638 MW;
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                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
 PRELIMINARY;
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                                                                                                                                      TISSUE=Lung carcinoma;
Polvi A., Ruosaari S.,
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                                                                                                                                                                                                                                                                                                                                                                                      Fas ligand (Fragment)
                                                                                                                                                                             Submitted (JUN-2003)
                                                                             (Human)
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E; PS00251; TN
E; PS50049; TN
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PD002012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                        63 AA;
                                                                                                                              FROM N.A
                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
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                                                                  Name=TNFSF10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P50591;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999
01-NOV-1999
01-OCT-2003
                                                                              Homo sapiens
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PROSITE;
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Best Local
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PRINTS;
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        Q6JSD9;
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                                                                                                                                                                                                                                                                                                                                                                                 -SSYLGAVFNFTSNDH
                                                                                                                                                QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK
                                                                                                                                                                                                                                                                                                  --SCN
                                                                                                                                                                                                                                                                                                                                                  165 DKQMVQYIY-KYTSYPDPILLMK-SARNSC-----WSKDAEYGLYSIYQGGIFELKENDR
                                                                                                                                                                                                                                                 105 NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
[1]
                                                                                                43;
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                                                                                                                                                                                                                                                                           --LEWEDT-YGISLISGVKYQKGGLVINDTGLYFVYSKIYFRGQ-
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                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
Spee B., Arends B., Favier R., Penning L.C., Rothuizen J.;
Spee B., Arends B., Favier R., Penning L.C., Rothuizen J.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX603042; AAT37155.1; -.

EMBL; AX603042; AAT37155.1; -.

HSSP; P01375; 1A8M.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006915; F:tumor necrosis factor receptor binding; II

GO; GO:0006915; P:mmune response; IEA.

GO; GO:0006915; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

InterPro; IPR008064; Fas_ligand.

InterPro; IPR008063; TNF_abc.

InterPro; IPR0080983; TNF_family.

InterPro; IPR008983; TNF_family.

InterPro; IPR008983; TNF_family.

InterPro; IPR008083; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor binding;
                                                Length
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 FDE395B014717B6B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27, Created)
27, Last sequence update)
27, Last annotation update)
                                Score 175.5; DB 2;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 163.5; DB 2; larity 27.1%; Pred. No. 1.1e-05; Conservative 32; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01681; FASLIGAND.
PRINTS; PR01234; TNECROSISECT.
PRINTS; PR01237; TNECROSISECT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
                                                                                               39;
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19274 MW;
                                                13.6%;
larity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
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PROSITE; PS50049; TNF 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Fas ligand (Fragment).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 LYVNVSELSLINFE
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                      94
                      -SSY
--WSKDAEYGLYSIY
                                                                                                                                                                                                                                                                                                                                                            nomas
                                                                                                                                                                                                                                                                                                             K.C.
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).

SUBUNIT: Homotrimer (Potential).

SUBCELLULAR LOCATION: Type II membrane protein (Probable).

TISSUE SPECIFICITY: Specifically expressed in endothelial cells.

Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.

SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                an
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     <u>18</u>
                                                                                                                                                                                                                                                                                                                                                            colon carc
                                                                                                                                                                                                                                                                                                              Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane
                                                                                                                                                                                                                                                                                  TISSUE=Umbilical vein;
MEDLINE=99091541; PubMed=9872942;
Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Cart. Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S., Li L.-Y., Gentz R., Yu G.-L.;
"VEGI, a novel cytokine of the tumor necrosis factor family, angiogenesis inhibitor that suppresses the growth of colon care
            Signal-anchor; Transmembrane.
Cytoplasmic (Potential).
Signal-anchor for type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (Potential).
Extracellular (Potential)
RFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMK-SARNSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005887; C:integral to plasma membrane; TAS GO:0005102; F:receptor binding; TAS. GO:000074; P:regulation of cell cycle; TAS.
                                           240
                                                                 129
                                                                95 LGAVFNLTSADHLYVNVSELSLVSFEESKTFFGLY
                                           OGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PR01234; TNECROSISFCT ProDom; PD002012; TNF_subf; 1
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                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50049; TNF 2; Glycoprotein;
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Genew; HGNC:11931; 7
MIM; 604052; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF
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85
                     48 RGQ---
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                                                                                                                        TN15 HUMAN
                                                                                                                                                                                                                                                                                                                                                                      vivo."
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                                           206
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                                                                                                                                 095150;
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                                                                                                             5 HUMAN
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ligands for herpesvirus entry mediator.";
Immunity 8:21-30(1998).
                                                                                                                                                                                                           116 WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--OM
                                                                                                                                                                                                                                                                                                               169 VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN
                                                                                                                                                                                                                                                                                                                                              -EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD
                                                                                                                                                                                                                                                            42 WE-HELGLAFTKNRMNYTNKFLLIPESGDYFIYSOVTFRGMTSECSEIRQAGRPNKPDSI
                                                                                                                                                          Gaps
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MEDLINE=21528948; PubMed=11673523;
Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
"Genomic characterization of LIGHT reveals linkage to an immune response locus on chromosome 19p13.3 and distinct isoforms generated by alternate splicing or proteolysis.";
J. Immunol. 167:5122-5128(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98122340; PubMed=9462508; DOI=10.1016/S1074-7613(00)80455-0.
Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=98438532; PubMed=9765287; DOI=10.1074/jbc.273.42.27548;
Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.
Tan K.B., Dede K., Spampanato J., Silverman C., Hensley P.,
DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
Truneh A., Young P.R.;
"Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for "Herpesvirus entry mediator ligand (T cells and inhibits HT29 cegrowth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 (Herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dove Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts
 (Potential) (Potential)
                                                                                                                                                         18;
                                                                                                         Length 174;
                                                                                                                                                          Indels
N-linked (GlcNAc. . .) (P. N-linked (GlcNAc. . .) (P. CCB83BA7EE673B98 CRC64;
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                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  043557; 075476; Q8WVF8; Q96LD2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member
mediator-ligand) (HVEM-L) (UNQ391/PRO726).
Name=TNFSF14; Synonyms=HVEML, LIGHT;
Homo sapiens (Human).
                                                                                                         1;
                                                                                      Score 160; Db 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA
                                                                                                                            ed. No. 3e-C
Mismatches
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                                                                                                                                                                                                                                                                                                                                           TVVITKVTDSYPEPTQLLMGTKSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                       24;
56 N
152 N
20131 MW;
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156 ISLVDYTKEDKTFFGAFLL
                                                                                                          12.4%;
35.3%;
                                                                                                                                                       Conservative
56
152
174 AA;
                                                                                                 Query Matcn
Best Local Similarity
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Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
 CARBOHYD
CARBOHYD
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                                                    SEQUENCE
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collaboration
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S.W.,
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                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length hum
                                                                                                       ns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse cDNA sequences.";
.. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFKB, stimulates the proliferation of T cells, and inhibits growth of the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
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         Xie M.-H., Yazz.
                                         Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I. Godowski P., Gray A.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2; Synonyms=LIGHT delta-TM;
IsoId=043557-2; Sequence=VSP 006452;
TISSUE SPECIFICITY: Predominantly expressed in the spleen busefound in the brain. Weakly expressed in peripheral lymphoid tissues and in heart, placenta, liver, lung, appendix, and kand no expression seen in fetal tissues, endocrine glands, or nonhematopoietic tumor lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a captiveen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                         Wieand D., Woods K., Xie M.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: N-glycosylated.
PTM: The soluble form of isoform 1 derives from tby proteolytic processing.
SIMILARITY: Belongs to the tumor necrosis factor CAUTION: Ref.5 sequence differs from that shown dframeshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: Up-regulated after T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence=Displayed;
                      C., Williams M., 3
                                                                                                                     bioinformatics assessment.";
Genome Res. 13:2265-2270(2003)
                                                                                                                                                                                (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; AF036581; AAC39563.1;
; AF064090; AAC25169.1;
; AY028261; AAK26160.1;
; AY358812; AAQ89171.1;
; BC018058; AAH18058.1; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=043557-1;
                           Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY028261; AAK2
EMBL; AY358812; AAQ8
EMBL; BC018058; AAH1
HSSP; P01375; 4TSV.
Genew; HGNC:11930; T
Vandlen R., war
Yu G., Yuan
Gray I
                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VQLGGVGCPLGLASTITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -IYKYT-SYPDPILLMKSARNSCWSKDAEYGLY
                                                                                                                                                                                                                                                            superfamily
                                                                                                                                                                                                                                                                                 superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVKWQLRQLVRKMILRTSEETISTVQEKQQN-ISPLVRERGPQRVAAHITGTRGRSNTLS
                GO; GO:0043027; F:caspase inhibitor activity; IDA.
GO; GO:00043027; F:caspase inhibitor activity; IDA.
GO; GO:0005102; F:receptor binding; IPI.
GO; GO:0006917; P:induction of apoptosis; TAS.
GO; GO:0001719; P:inhibition of caspase activation; IDA.
GO; GO:0007165; P:signal transduction; NAS.
GO; GO:0043029; P:T-cell homeostasis; NAS.
GO; GO:0042098; P:T-cell proliferation; NAS.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF subf.
                                                                     IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

NCBI TaxID=9544;
                                                                                                                                                                                                                                                                                                                    membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             240;
                                                                                                                                                                                                                                     Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LLWE-TQLGLAFLRGLSYHDGALVVTKAGYYYIYSK-
                                                                                                                                                                                                                                                           ligand
                                                                                                                                                                                                                                                                     member 14, membrane form.
Tumor necrosis factor ligand
member 14, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
Signal-anchor for type II m
protein (Potential).
Extracellular (Potential).
Cleavage (Potential).
Potential.
N-linked (GlCNAc. . .).
Missing (in isoform 2).
/FIId=VSP_006452.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                            necrosis factor
                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 159.5; DB
Pred. No. 5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 5e-0
Mismatches
                                                                                                                                                 InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF 2; 1.
Alternative splicing; Cytokine; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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퍼
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(TrEMBLrel. 22, I
(TrEMBLrel. 25, I
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Similarity 23.8%;
53; Conservative
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214
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187
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HIX0019691;
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214
240 AA;
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Q8MJ19;
01-OCT-2002 (TrEMI
01-OCT-2003 (TrEMI
01-OCT-2003 (TrEMI
Fas ligand CD178
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                                                                                                                                                                                                                                               Transmembrane
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DISULFID
CARBOHYD
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TRANSMEM
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                           MEDLINE=22937400; PubMed=14576776;
Arnoult D., Petit F., Lelievie J.D., Lecossier D., Hance A.,
Monceaux V., Ho Tsong Fang R., Huntrel B., Ameisen J.C., Estaquie
"Caspase-dependent and -independent T-cell death pathways in
pathogenic simian immunodeficiency virus infection: relationship
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                        factor receptor binding;
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                                                                                                                                                                                             Hance A.J., Lecossier D., Estaquier J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                971A43779E029449 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member
Name=Thfsf14; Synonyms=LIGHT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%; Score 157; DB 2; 27.4%; Pred. No. 4.5e-05
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C: GO: 0016020; C:membrane; IEA.
C: GO: 0016020; C:membrane; IEA.
C: GO: 0006916; F:tumor necrosis factor of GO: 0006915; F:mmune response; IEA.
C: GO: 0007165; P:immune response; IEA.
C: GO: 0007165; P:signal transduction; IEA.
C: GO: 0007165; P:signal transduction; IEA.
C: GO: 0007165; P:signal transduction; IEA.
C: GO: 0007165; F:signal transduction; IEA.
C: GO: 0007165; F:sign
                                                                                                                       disease progression.";
Cell Death Differ. 10:1240-1252(2003)
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HSSP; P50591; 1D2Q.
GO; GO:0005576; C:extracell
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FE; PSO0251; TNF 1; 1.

FE; PSS0049; TNF 2; 1.
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Mammalia; Eutheria;
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PROSITE;
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Pfam; PF0
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMBL; AR029155; BAA88559.1; -..

REMBL; AF227533; AAF36722.1; -..

REMBL; AF227533; AAF36722.1; -..

REMBL; AF227533; AAF36722.1; -..

ROS; GO:00043027; F:caspase inhibitor activity; ISS.

GO; GO:0001719; P:inhibition of caspase activation; ISS.

GO; GO:0001719; P:receptor binding; ISS.

GO; GO:0001719; P:release of cytoplasmic sequestered NF-kappaB; ISS.

GO; GO:00043029; P:T-cell homeostasis; ISS.

GO; GO:0042098; P:T-cell proliferation; ISS.

ROS; GO:0042098; P:T-cell proliferation; ISS.

RILETPRO; IPR006053; TNF_family.

RILETPRO; IPR008983; TNF_family.

RILETPRO; IPR008983; TNF_like.

RILETPRO; IPR003636; TNF_subf.
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NFKB
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                                                                                                                                                                                                          TISSUE=Lymphoma;
Force W.R., Todd P.K., Mikayama T.;
Force W.R., Todd P.K., Mikayama T.;
Force W.R., Todd P.K., Mikayama T.;
"Mouse LIGHT; molecular genetics, ligand binding and expression at LIGHT; molecular genetics, ligand binding to Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to decoy receptor TNFRSF6B modulates its effects. Activates N stimulates the proliferation of T cells.
stimulates the proliferation of T cells.
-!- SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).

PTM: The soluble form derives from the membrane form by proteolytic processing.

SIMILARITY: Belongs to the tumor necrosis factor family
                                                                        Kitamura T.;
a mouse homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor; Transmembrane.
Tumor necrosis factor ligand
member 14, membrane form.
Tumor necrosis factor ligand
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Extracellular (Potential).
Cleavage (Potential).
Potential.
N-linked (GlCNAc. . .) (Pot
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Cytoplasmic (Potential).
Signal-anchor for type II
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No. 0.00019;
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SEQUENCE FROM N.A.
TISSUE=Fetal liver;
MEDLINE=20354998; PubMed=10894944;
Misawa K., Nosaka T., Kojima T., Hirai M., I
"Molecular cloning and characterization of i
TNFSF14, a member of the TNF superfamily.";
Cytogenet. Cell Genet. 89:89-91(2000).
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5; Mismatches
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ProDom; PD002012; TNF subf; 1.
PROSITE; PS00251; TNF 1; FALSE
PROSITE; PS50049; TNF 2; 1.
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LIRAA
-LLWE-TRLGLAFLRGLTYHDGALVTMEPGYY
                                                   RVWWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PILLMKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YEPDVSKNNIDWKQNQDGAFVSGGLKLVDR
                               YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLY-
                                                                                                                                                                                                                                                                                                                        rpio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Cyprinus.

NCBI TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVF
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE=Head kidney;

TISSUE=Head kidney;

PubMed=15145420; DOI=10.1016/j.fsi.2003.11.001;

Ravan R., Sakai M.;

"Presence of multiple isoforms of TNF alpha in carp (Cyprinus car L.): genomic and expression analysis.";

L.): genomic and expression analysis.";

Fish Shellfish Immunol. 17:87-94(2004).

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.

R InterPro; IPR006983; TNF family.

InterPro; IPR008983; TNF like.

InterPro; IPR008983; TNF subf.
                                                   140 YVYSKVQLS-GVGCPQGLANGLPITHGLYKRTSRYPKELELLVSRRSPCGRANSS
                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                            239
                                                                       SIYQGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  010BC2B1E8D7265E CRC64;
                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor-alpha (Fragment).
Mesocricetus auratus (Golden hamster).
                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 151.5; DB 2;
Pred. No. 0.00021;
1; Mismatches 68;
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                                                                                                                                                                  Created)
                                                                                                                                             PRT;
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25226 MW;
                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, C
01-OCT-2003 (TrEMBLrel. 25, L
01-MAR-2004 (TrEMBLrel. 26, L
Tumor necrosis factor-3 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; 25.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     subf;
           AAHLTGANASLIGIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                             PRELIMINARY;
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, TNF gr
TNF;
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Name=TNF-3alpha;
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PD002012; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00207; TN
E; PS50049;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229;
                                                                                                                                                       Q7T2Q3;
01-OCT-2003
01-OCT-2003
01-MAR-2004
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O70332;
01-AUG-1998
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PROSITE;
SEQUENCE
                                                                       203
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            93
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor alpha.

Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Moronidae; Lateolabrax.

NCBI_TaxID=8164;
                                                                                                                                                                                                                            CDNAS
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                          Cricetinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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                                                                                                                                                                                                    , Freeman G.L.;
s auratus) cytokine
experimental visce
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Qiu L., Song L., Wu L., Cai Z., Xu W., Wang L.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY376595; AAR02413.2; -.

HSSP; P01375; 1A8M.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding;
                                                                                                                                                                                                                                                                                                                                                                                                        factor receptor binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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  Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - ITGTRGRSNTL - SSPNSKNEKALGRKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144.5; DB 2;
Pred. No. 0.00074;
3; Mismatches 63;
                                                                                                       SEQUENCE FROM ....
SEQUENCE FROM ....
TISSUE=5pleen;
MEDLINE=98234044; PubMed=9573100;
Melby P.C., Tryon V.V., Chandrasekar B., Fr
"Cloning of Syrian hamster (Mesocricetus au "Cloning of Syrian hamster (mesocricetus au "Cloning of Syrian hamster (mesocricetus au "Loning of Syrian hamster (mesocricetus au "Loning")
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                                                                                                                                                                                                                                                                                              Infect. Immun. 66:2135-2142(1998).
EMBL; AF046215; AAC40100.1; -.
HSSP; P06804; 2TNF.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis fact
GO; GO:0006955; P:immune response; IE
InterPro; IPR006053; TNF abc.
InterPro; IPR002959; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF family.
InterPro; IPR008983; TNF subf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNFALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subf; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23793 MW;
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Similarity 26.9%;
47; Conservative 2
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    Mammalia; Metazoa; (Mammalia; Eutheria; F
Mesocricetus.
NCBI_TaxID=10036;
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216 AA;
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PS50049; T
231 AA;
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232
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01-JUN-2003
01-OCT-2003
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               PROSITE;
SEQUENCE
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Best Local S
Matches 45
                                                                                                                                     93
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SEQUENCE
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                                              Query Match
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                    SARNSCWSKDAE----YGLY-SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA
                                                                                                                                                                                                               I-SNLH
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

TISSUE=Head kidney;

MEDLINE=22365628; PubMed=12477499; DOI=10.1016/S0145-305X(02)000
Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,

Wiegertjes G.F.;

"Molecular and functional characterization of carp TNF: a link b
TNF polymorphism with trypanotolerance?";

Dev. Comp. Immunol. 27:29-41(2003).

EMBL; AJ311801; CAC84642.2; -.
                                                                                                                                                                                                              LVRERGPQRVAAHITGTRGRSNTLSS----PNSKNEKALGRKINSWESSRSGHSF1
                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                        LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEA
                                                                                                                                                                     241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor receptor binding;
                                                                                                                                                                                         Indels
                                                                                                                                                                    Length
                                                                                                                                               2C493CF80651EA2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Putative Tumour necrosis factor alpha two.
                                                                                                                                                                                        87;
                                                                                                                                                                   11.1%; Score 143; DB 2; 24.3%; Pred. No. 0.0011;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          231
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                IEA
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GO; GO:0005164; F:tumor necrosis fact
GO; GO:0006955; P:immune response; IE
InterPro; IPR006053; TNF_abc.
InterPro; IPR006050; TNF_beta.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_like.
              P:immune response;
GO; GO:0006955; P:immune terror interPro; IPR006053; TNF abc.
InterPro; IPR002960; TNF beta.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR008983; TNF subf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01236; TNFBETA.
ProDom; PD002012; TNF subf; 1.
                                                                                                                                                                                        34;
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                                                                                                                                    NF 2; 1.
26702 MW;
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                                                                                                                                                                                          Conservative
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                                                                                                                  SMART; SM00207; TNF; 1
PROSITE; PS50049; TNF
GEOTTENCE 241 AA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=TNF-alpha2pro;
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 44; Conser
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                                                                                                                                                                                                                                                                             153 RFQEEIKENTKNDKQMV-----QYIYKYTSYPDPILLMKSARNSC-WSKDAEYGLY-S
                                                                                                                                                                                                                                                                                                                 136 HI--SCKHDMTEDODVVHMSHAVLRYSESYGSYKP---LFSAIRSACVHASDSEDLWYNT
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                                                                                                                               --ISPLVRERGPORVAAHITGTR
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Green R.M., Herbst M.M., Schountz T.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY249143; AAP03078.1; -.

HSSP; P06804; 2TNF.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

InterPro; IPR006053; TNF_abc.

InterPro; IPR006052; TNF_family.

InterPro; IPR006052; TNF_family.

InterPro; IPR008983; TNF_like.

InterPro; IPR003636; TNF_subf.
                                                          231;
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                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 Potential.
>232 tumor necrosis factor.
232
25704 MW; E48A9379DB4F216D CRC64;
                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                                                     IYOGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 137.5; DB 2;
larity 24.5%; Pred. No. 0.003;
Conservative 36; Mismatches 78;
                   2AD8871D0B1A82F1
                                                      Score 141; DB 2;
Pred. No. 0.0016;
3; Mismatches 9(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor necrosis factor precursor (Fragment)
                                                                                                                              44 WOLROLVRKMILRTSEETISTVQEKQQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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PRINTS; PR01235; TNFALPHA.
ProDom; PD002012; TNF_subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
                                                                                           38;
TNF 2; 1.
25927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 24, (TrEMBLrel. 24, 1)
                                                                                                                                                                                                                                          ---YDPDVCKDNL---
                                                    / Match
Local Similarity 23.3%;
les 51; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00229; TNF;
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Fri

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PIR; A25453,
HSSP; P06804; 2TNF.
InterPro; IPR006053; T
InterPro; IPR008983; T
InterPro; IPR008983; T
                                                                                                                                                                                                                      5:157-165 (1986)
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                   TNF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
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SYPDP 181
                SYEDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EHL--
                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                          HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-T
                 -GCSNYVLLTHTVSRFAV
                                --LYSIYQGGIFELKENDRIFVSVTNEHLIDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 YKYT-SYPDPILLMKSARNSCWSKDAEYGLY--SIYQGGIFELKENDRIFVSVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GYNSES-
                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                     GO:0016020; C:membrane; IEA.
GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO:0006955; P:immune response; IEA.
erPro; IPR006053; TNF abc.
erPro; IPR002960; TNF beta.
erPro; IPR006052; TNF family.
erPro; IPR008983; TNF family.
erPro; IPR008983; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                           6E88DCF46D3F131C CRC64;
                                                                                                                                            27, Created)
27, Last sequence update)
27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLHKTQGNQQDGSVLRLTLRDRISQGNFTSKAAIHLTG--
                                                                                                                                                                                                                                                                                                                                                                                                           Score 137.5; DB 2;
Pred. No. 0.0031;
0; Mismatches 83;
                                                                                                                                                                                                                                     Phelan P.E. III, Mellon M.M., Kim C.H.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ
EMBL; AY427649; AAR06286.1; -.
HSSP; P01375; 1A8M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA.
          ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                ILLMKSARNSCWSKDAEYG--
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01234; TNECROSISFCT PRINTS; PR01236; TNFBETA.
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                                                                                                                                                                                                                                                                                                                                                                                         25826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            10.7%;
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VENDNGKTFFGVF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           234 AA;
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00207; TI
PROSITE; PS50049;
                                                                                 228 VYFG 231
                                                                                                                                                                                                                               FROM N.A
                                                                 - FFG
                                                                                                                                            05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                               SEQUENCE
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P04924;
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                                                                                                           RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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ill health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding for rabbit tumor necrosis factor.";

LONA 5:149-156(1986).

-I- FUNCTION: Cytokine that binds to TNFRSFIA/TNFR1 and TNFRSFIB/TNFBR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, Under certain conditions it can stimulate cell proliferation and induce cell differentiation.

-!- SUBUNIT: Homotrimer (By similarity).

-!- SUBCELULAR LOCATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity).

-!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-!- PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By initialization).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=91065534; PubMed=2249779; DOI=10.1016/0378-1119(90)90364-W,
Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
Nedospasov S.A.;
"Structural analysis of the rabbit TNF locus, containing the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exists as
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                                                                                                                            (Tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω.¥.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene encoding rabbit tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing the (tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Todd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9137;
S., Sakamoto H., Kajihara J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases, i
by general
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Wallace R.B.; "Molecular cloning of the gene encoding rabbit tumor ne
                                                                                                                                                                                                                                                                                         Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86219711; PubMed=3519137;
Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara Hayashi H., Kato M., Seko M.;
"Molecular cloning and expression in Escherichia coli coding for rabbit tumor necrosis factor.";
                                                                                                                                                                                                                                               Craniata, Vertebrata;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Tumor ligand superfamily member 2) (TNF-a) (Cachectin).
Name=TNF; Synonyms=TNFA, TNFSF2;
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Cachexia accompanies a variety of and infection, and is characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is of the rabbit TNF locus, (lymphotoxin) and TNF-alpha
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SEQUENCE FROM N.A.
MEDLINE=86219712; PubMed=3519138
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TNF family.
TNF like.
TNF subf.
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EMBL; M12846; AAA31482.1;
EMBL; M60340; AAA31484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95:215-221 (1990)
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DR PFEAM; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISECT.

DR PRODOM; PD002012; TNF subf; 1.

DR SMART; SM00207; TNF 1.

DR PROSITE; PS0049; TNF 2; 1.

DR PROSITE; PS0049; TNF 2; 1.

KW Cytokine; Phosphorylation; Signal-anchor; Transmembrane form.

FT CHAIN 1 235 Tumor necrosis factor, membrane form.

FT CHAIN 35 Tumor necrosis factor, membrane form.

FT CHAIN 36 56 Signal-anchor for type II membrane form.

FT DOMAIN 57 235 Extracellular (Potential).

FT SITE 79 80 Cleavage (by ADAMI7) (By similarity).

FT MOD RES 2 2 Phosphoserine (by CKI) (By similarity).

FT DISULFID 148 179 By similarity.

FT CONFLICT 63 63 Missing (in Ref. 3).

Ouery Match 10.6%; Score 136.5; DB 1; Length 235;
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ILLMKSARNSCWSKDAEYG----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235 -WESSRSG 122 123 HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 181 Gaps Indels 72 ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS--Query Match
Best Local Similarity 23.0%; Pred. No. 0.0037;
Matches 42; Conservative 37; Mismatches 81; 238 231 FFG 114 182 236 229 Q g <u>გ</u> 8 ઠે ਠੇ ઠે

Search completed: June 3, 2005, 06:43:56 Job time : 176 secs This Page Blank (uspto)

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Compugen Ltd.
 GenCore version (c) 1993 - 2005
            Copyright
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protein search, using sw model OM protein

; Search time 161 Seconds
 (without alignments)
583.744 Million cell upda 2005, 06:25:45 , М June . ::00 Run

tes/sec

243

281 Title: Perfect score:

... NEHLIDMDHEASFFGAFLVG US-10-662-431-2_COPY_39_1287 1 TNELKQMQDKYSKSGIACFL.. Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

386760381 residues 2105692 seqs, Searched:

1523986 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 243

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Genesed Database

Geneseq_16Dec04:*
geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003as:* 40m4m9r8

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	uo	Human TRA	ell f	artia	Human TRA	Human TNF	Partial h	mino aci	TRAIL ami	-termina	TNF famil	Tumour ne	Human TRA		Cat solub	at solub	luman TRA	Polypepti	og solub	og solub	Amino aci	Human TNF	Human sec	Human TRA	Human TNF	Human TRA
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SUMMARIES	ID	ADN35127	AAY88630	ABG72258		989	ABG72259	AAB08274	8440	AAY71985	3985		AAU99301	30	AD024774	17	AAU79599	51	2477	AD024772	AAB08275	8	AAG03752	AAU79600	ADL98267	AAU79595
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RESULT 1 ADN35127						
ID ADN3	5127	standard;	protein;	in;	187 AA.	
C ADN3512	15127;					
17	-JUN-2004	(first	t entry	<u>\$</u>		
DE Human	in TRAI-1	extra	extracellular		region.	
W human'	ın TRAI-1	extra	racellul	Ä	region; antineoplastic.	
S Homo	sapiens					
	CN1436792-A.					
20	-AUG-2003.					
08	-FEB-2002;	2002	2002CN-00104519	451	. 6	
08	-FEB-2002;	2002	2002CN-00104519	451	. 6	
A (PREC-)	C-) INST		PRECLINICAL		MEDICINE CHINESE ACAD M.	
I Zheng	ıg D, Liu	u Y,	Shi J;			

The present invention provides one kind of mutant 95-281 recombinant soluble polypeptide (rsTRAILthr95gly-281) in human TRAIl extracellular region. The preparation process and antineoplastic application of the recombinant soluble polypeptide are also provided. The present sequence represents human TRAI-1 extracellular region. Chinese. 1; 15pp; ID NO 187 AA; Claim 1; SEQ Sequence

ligand antineoplastic

factor relative cell death inducing on mutation polypeptide, used for an

New tumor necrosis fa extracellular region application.

2004-023846/03

WPI;

Length 187 Indels 2; .. σ Query Match

74.4%; Score 958; DB 8
Best Local Similarity 98.9%; Pred. No. 3e-85;
Matches 184; Conservative 0; Mismatches 0;

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117 58 SEETISTVOEKOONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE

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Pred. No. 1.1e-84;
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The present invention relates to the isolation of cDNA encoding human tummour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Trail109, and Trail114 proteins, and may be useful in a new preparation for killing tummour cells. The present sequence represents the partial human Trail protein,
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Pred. No. 2.7e-80;
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tem; tumour cell
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109
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ABG72258 standard; protein; 173
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172; Conservative
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Sequence 168 AA;
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                                                                                   Human; TRAIL; tumour necrosis factor; TNF;
tumour necrosis factor related apoptosis inducing ligand; TRAIL
viral infection; cytostatic.
                                                                                                                                                                                                                                        Producing and crystallizing tumor necrosis factor related apoptor inducing ligand protein, and its three-dimensional structure.
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N-PSDB; ABL53366.
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Best Local Similarity
Matches 168; Conser
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                                                                                                                 Homo sapiens
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This invention relates to an expression vector containing the tumour necrosis factor related apoptosis inducing ligand (TRAIL) protein receptor SDRS. The invention also comprises a method for producing the receptor SDRS. The invention also comprises a method for producing the sDRS protein from an E. coli transformed with the vector. The method of the invention is useful for crystallising the recombinant proteins i.e. proteins with improved stability or cytotoxic activity of a TRAIL protein which involves changing the amino acid of the AA loop to increase the various interactions between amino acids or from the binding site of metal ions or the disulfide bonding, or changing the corresponding amino acids of the homotrimer interface or homodimer interface to increase the various interactions between amino acids or from the binding site of metal ion or disulfide bond, or to fill the cavity. A 3 dimensional structure of the TRAIL-SDRS complex is useful for the molecular strategy conferring specificity for the recognition between TNF family members and TNF receptor family members and for the development of TRAIL protein, which has a better stable, cytotoxic activity or an improved receptor binding affinity. The present sequence represents the human tumour cerosis factor receptor apoptosis including ligand (TRAIL) protein sequence used in the invention
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SDR5; complex; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel expression vector containing an sDR5 encoding gene transformed Escherichia coli to produce sDR5 protein for crystallizing a tumor necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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including ligand; human l structure; TRAIL-SDR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; I
2.3e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                             Lim KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 887;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           Yoon JI,
                                                                                                                                                                                                                                                                                                                                                        & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
 TNF receptor apoptosis in necrosis factor; crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.9%; SC.
100.0%; P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                           Hwang YH,
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POHANG SCI
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Best Local Similarity
Matches 168; Conser
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Unidentified
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Best Local S
Matches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR84402;
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                            Boyle
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                                                                                                                                                                                                                                                                            The present invention relates to the isolation of cDNA encoding human tummour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Trail109, and Trail114 proteins, and may be useful in a new preparation for killing tummour cells. The present sequence represents the partial human Trail protein,
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                                                                                                                                                                                                                                      expression protein and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                  Length 168;
                                 Trail114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                         death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA
                                 ; tumour related apoptosis inducing ligand; prokaryotic expression system; tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                Score 882; DB 5; |
Pred. No. 7.2e-78; |
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human TNF ligand TRAIL.
                                                                                                                                                                                                                                                               (disclosure); 17pp; Chinese.
                                                                                                                                                                            COLLEGE PLA.
                                                                                                                                                                                                                                        gene
                                                                                         /note= "Encoded by CTT"
                 Trail114
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                        gene,
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                                                                                                                                                                            MILITARY MEDICAL
                                                                                                                                                            2001CN-00132371.
                                                                                                                                                                                                                                      induction ligand
                                                                                                                                                                                                                                                                                                                                                                                                68.5%;
nilarity 99.4%;
Conservative
                 protein,
                                                                                                                                           2001CN-00132371
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                  104
                 Trail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                             2002-751439/82
                                                                                                                                                                                                                                             preparation method
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 167; Conser
                                                                                                                                                                                                                      N-PSDB; ABX14393.
                                                                                                                                                                                                                                                               7; Page 10
                                                                                                                                                                                                                                                                                                                                                                                  168 AA;
                                                                                 Misc-difference
                 Partial human
                                                                                                                                           30-NOV-2001;
                                                                                                                                                            30-NOV-2001;
                                                                                                                                                                            (TWOM-) NO 2
                                                          sapiens
                                                                                                                                                                                                                                       death
                                                                                                           CN1354183-A
04-MAR-2003
                                                                                                                           19-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                          cells. The Trail114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08274;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                 Human;
                                           Trail
                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                        Tumor
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                                                          Ношо
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<del>a</del>
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197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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 disease;
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te disorders,
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0
AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's distype II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis; lupus and graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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and immune
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Pred. No. 1.7e-77;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptides comprising tumor necrosis proteins, useful for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.2%; Sc
larity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Fig 9; 71pp; English.
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99US-0166271P
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rheumatoid arthritis.
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166; Conser
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                                                                                                                                                                                                                                                                            11-FEB-2000;
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                             12-FEB-1999;
18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;

Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;

therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;

haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;

post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                               tumor
                                                                                                                                                                                                                                                                                                                               ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWS
                                                                                                                                                                                                                                                                                              75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                             Gape
                                                                                                                                     ٦ E
                                                                                                                                                                                     The invention relates to a TNF-related apoptosis-inducing ligand (TRAIL) cDNA and its encoded polypeptide. The gene of the inventirelated to mutational human tumour necrosin. The polypeptide of tinvention is useful for inducing the death of tumour cells. The sequence represents the TRAIL amino acid sequence
                                                                                                                                     polypeptide, usefuto musefu
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                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                            Length 167;
                                                                                                                                                                                                                                                                                                                                                               KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                            Score 866; .DB 6;
Pred. No. 2.6e-76;
                                                                                                                                     cDNA and encoded
                                                                                                                                                                                                                                                           · DB
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal region of human TRAIL protein.
                                                                           CO LTD
                                                                                                                                                                                                                                                                    No.
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                                                                                                                                     Death induced ligand (TRAIL) cDNA inducing the death of tumor cells, necrosin.
                                                                                                                                                                                                                                                                                                                                                                                                                             Z
                                                                          (CHEN-) CHENGDU DIAO PHARM GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71985 standard; protein; 161
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                      14pp; Chinese.
                                         2001CN-00105946
                                                          2001CN-00105946
                                                                                                                                                                                                                                                           67.3%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32. .34
/label=
                                                                                                           WPI; 2003-230973/23.
N-PSDB; ACC83357.
                                                                                            Liu
                                                                                                                                                                                                                                                                    1 Similarity 166; Conser
                                                                                                                                                                                                                                           Sequence 167 AA;
                                                                                                                                                                       7
                                                                                            Gao X,
                                                                                                                                                                      Claim 4; Fig
                                       10-APR-2001;
                                                         10-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
       CN1380339-A
                        20-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71985;
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                                                                                                                                                                                                                                                                                                                                135
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                                                                                                                                                                                                                                                            Query Match
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FIRENCE
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The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a C-terminal region of human TRAIL protein. which has 20-25% sequence identity with the C-terminal region of human TALL-1 protein extracellular domain. TRAIL protein is a TNF family member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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Pred. No. 9.2e-75;
0; Mismatches 0;
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                                                                                                                                                                                                         /label= Beta_strand
99. .109
/label= Beta_strand
118. .128
/label= Beta_strand
                                                                                           Beta_strand
                                                                                                                                                               'label= Beta_strand
                                                                                                                                                                                                                                                                                                                                                                                                      Beta_strand
                                                                                                                                                                                                                                                                                                           Beta_strand
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100.0%; Pr
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2000US-0201012P
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/label=
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                                                       17. .50
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42. .4,
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47. .5
                                                                                                                                                                        /lat
86.
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hes 161; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999;
01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to RANK or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a composition (I) comprising a protein compine crystalline form, where the complex comprises an amino acid sequence a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL) ectodomain. (I) is useful for identifying a compound with RANK modulactivity, and for identifying a RANK or OPG modulating compound. (I) useful to intelligently design mutants that have altered biological properties and for identifying and/or designing compounds that bind as an approach towards developing new therapeutic agents. (I) is als useful to computationally screen small molecule databases for chemic entities or compounds that can bind in whole, or in part, to RANK or RANKL. The present sequence represents a tumour necrosis factor (TNE family member, TRAIL (1d4v), used in a structural-based alignment st
                                                                                                                                                                                                 of necrosis factor kB; RANK ligand; RANKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
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                                                                                                                                                                                                                                                                                                                                                                                                               Fremont DH;
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                          161
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SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                       (1d4v) protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        re 850; DB 6;
red. No. 9.2e-75;
Mismatches 0;
                                                                                                                                                                                                              TNF; TRAIL; cytokine.
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                                                                                                                                                                                                                                                                                                                                                                                                               Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Teitelbaum SL,
                                                                                          standard; protein; 161
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                                                                                                                                                                                                                                                                                                                                                                                     (BARN-) BARNES-JEWISH HOSPITAL
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                                                                                                                                                                                                                                                                                                                                             2001US-0311163P
2002US-00105057
                                                                                                                                                                                                                                                                                                                    2002WO-US025287
                                                                                                                                            (first entry)
                                                                                                                                                                       TRAIL
                                                                                                                                                                                                activator
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                                                                                                                                                                                                              tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     murine RANKL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-256526/25.
                                                                                                                                                                       family member,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             FP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 161 AA;
                                                                                                                                                                                                                                                                WO2003014077-A2
                                                                                                                                                                                                 receptor
                                                                                                                                                                                                                                                                                                                                           09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                Ross
                                                                                                                                                                                                                                                                                                                                                         22-MAR-2002;
                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                   09-AUG-2002;
                                                                                                                                             11-AUG-2003
                                                                                                                                                                                                                                                                                           20-FEB-2003
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                                                                                                                    ABR39855;
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203
                         121
                                                                                          ABR39855
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                                                                                                                                                                                                 RANK;
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Matches
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The invention relates to a composition comprising a protein complex in crystalline form, where the complex comprises an amino acid sequence of a receptor activator of nuclear factor kappaB (NFkappaB) (RANK) ligand (RANK) ectodomain. The three-dimensional structural representation of a RANK ectodomain crystal complex, is useful for identifying a RANK or osteoprotegerin (OPG) modulating compound, and for identifying a RANK or with RANK modulating activity. The crystals permit the determination of the three-dimensional X-ray diffraction structure of the crystal-line polypeptide to high resolution. The atomic structure coordinates and structural information which comprises atomic structure coordinates are useful for identifying bone-forming compounds by methods which utilise the coordinates for solving the three-dimensional X-ray diffraction and/or solution structural information may also be used in a variety of molecular modeling and computer-based screening applications, to for example design mutants of the crystallized RANKL, its receptors, or a portion or fragment of RANKL or its receptors. The coordinates of RANKL crystal, are useful for designing or identifying candidate compounds capable of modulating RANK biological activity, and for identifying compounds which mimic the capability of RANKL to bind RANK molecules, thereby activating the tumour necrosis factor family cytokine, TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of NFkappaB (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                               nain crystal complex; RANK; osteoprotegerin; OPG; compound; tumour necrosis factor; TNF family; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising crystalline receptor activator of NFkappaligand ectodomain complex whose three-dimensional structural representation is useful for identifying RANK or osteoprotegrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fremont DH;
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Pred. No. 9.2e-75;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelson
                                                                                                                               cytokine,
                                                                                                                                                          ectodomain crystal complex; RANK;
                                ADC03335 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teitelbaum SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Sit; Conservative 0;
                                                                                                                               family
                                                                                                                                                                                                                                                                                                                             2002US-00215446
                                                                                                                                                                                                                                                                                                                                                             2001US-0311163P
                                                                                               (first entry)
                                                                                                                                 factor
                                                                                                                                                                                                                                                                                                                                                                                                           ROSS F P.
TEITELBAUM S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FREMONT D H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AA;
                                                                                                                                 necrosis
                                                                                                                                                                                                                                                              US2003050223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           NELSON
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                                                                                                                                                                              bone-forming
                                                                                                                                                                                                                                                                                                                            09-AUG-2002;
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                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                              13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulating
                                                                ADC03335;
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Best Local
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(FREM/)
                                                                                                                                                                                                                                                                                                                                                                                                           (ROSS/)
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                                                                                                                                 Tumour
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                                                                                                                                                                RANKL
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RESULT
ADC0333
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The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain
                                                                           120
                                                     202
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                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                               Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26; rpl-6-6.
             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New splice variants of tumor necrosis factor-related apoptosis i
ligand (TRAIL) isolated from B-lymphocytes and liver, useful to
diseases or disorders associated with low expression of the vari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by in-frame stop codon"
                                                                                                    SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                                                                                                        rpl-6-6, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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::
                                                                                                                                                                                            AAU99301 standard; protein; 212
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                                                                                                                                                                                                                                                                         variant
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39. 21
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                                                                                                                                                                                                                                                                      splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YELI/) YELIN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002061525-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2002.
                                                                                                                                                                                                                                                                         TRAIL
                                                                                                                                                                                                                                               24-SEP-2002
                                                                                                                                                                                                                     AAU99301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                          Human
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containing receptors, DR4 and DR5, as well as two decoy receptors, DCR1 and DCR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/ining and activity.

Cheir cellular distribution of spression levels/ining and activity.

Cheir cellular distribution be used in gene therapy, to raise antibodies, to induction of apoptosis of tumours cells. The splice variant polypeptides and polymucleotides can be used in gene therapy, to raise antibodies, to expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression of the amino acid sequences are useful for causing a cyctoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic the amino acid sequences. The antibodies may also have a therapeutic products. Diseases that may be treated include cancer, neurodegenerative development of tissues and aging TRAIL's gene is located on chromosome addisorned (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-terminal section of the conserved TNP domain deleted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWOVKWOLROLVRKMILRTSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 827; DB 5;
Pred. No. 2.4e-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .154
/note= "X shown in !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TRAIL protein (aa 119-281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 154
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91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 212 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003050134-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158;
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Best Local S
Matches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
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nematosus;
sting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                   compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                    ψ
                                                                                                                                                              that bind, inhibit or mimic a Neutrokine-alpha protein or enhanc activity of a Neutrokine-alpha protein for treating e.g. cancer allergic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; dermatological; antirheumatic; antiarthritic; neuroprotective; canine; feline; TNF-related apoptosis-inducing TRAIL; apoptosis; cancer; neurodegenerative disease; lupus eryth rheumatoid arthritis; multiple sclerosis; diagnosis; genetic tes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                                                                                                                   crystalline Neutrokine-alpha protein, useful for designing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 764.5; DB Pred. No. 2e-66; ); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       human neutrokine-alpha protein (ADI53050).
                                                                                        Volovik Y;
                                                                                                                                                                                                                            Disclosure; Fig 1; 362pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO24774 standard; protein; 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                             2001US-0331049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.4%;
ilarity 90.8%;
Conservative (
2002WO-US035661
                                                           SCI INC
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                                                                                       Arnold E,
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                                                           (HUMA-) HUMAN GENOME
                                                                                                                     WPI; 2003-532895/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 148; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154 AA;
                                                                                        Oren DE,
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07-NOV-2002;
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                             07-NOV-2001;
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                                                                                                                                                                               activity
allergic
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                                                                                     Li Y,
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134
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neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;
TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;
rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                             a canine
                                                                                                                                                                                                                                   (I)
The
                                                                                                                              ligand and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELVIHEKGFYYIYSQTYFRFQ--EEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide (I) comprising a car or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and optionally a fusion peptide fused to the polypeptide. Modulators of (are useful for treating an apoptosis-related disorder in a subject. I apoptosis-related disorder is chosen from cancer, neurodegenerative disease, lupus erythematosus, rheumatoid arthritis and multiple sclerosis. (I) is useful for diagnostic evaluation, genetic testing and/or prognosis of angiogenesis-related disorders, such as cancer. T sequence represents a gene encoding a cat soluble TRAIL protein used the invention.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                             Novel isolated canine or feline TNF-related apoptosis-inducing polypeptide, useful for diagnostic evaluation, genetic testing prognosis of angiogenesis-related disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                171;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRAIL with a C-terminal V5-His tag protein.
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Pred. No. 2.6e-66;
                                                                                                                                                                                  Disclosure; SEQ ID NO 29; 151pp; English
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                                                                                                                                                                                                                                                                                                                                                                              59.4%; illarity 84.2%; Conservative 13.
             2002US-0422342P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD024776 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                       INC.
                                      (PFIZ ) PFIZER PROD
                                                                                         2004-376043/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                     N-PSDB; ADO24773
                                                                                                                                                                                                                                                                                                                                                      Sequence 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004039307-A2
                                                                Rong
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             30-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                         144;
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Best Local
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                                                                GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                Cai
                                                                                          WPI
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<del>d</del>
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The invention relates to an isolated polypeptide (I) comprising a canine or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and optionally a fusion peptide fused to the polypeptide. Modulators of (I) are useful for treating an apoptosis-related disorder in a subject. The apoptosis-related disorder is chosen from cancer, neurodegenerative disease, lupus erythematosus, rheumatoid arthritis and multiple sclerosis. (I) is useful for diagnostic evaluation, genetic testing and/or prognosis of angiogenesis-related disorders, such as cancer. This sequence represents a gene encoding a cat TRAIL protein with a V5-His Tag at the C-terminus and used in the invention.
                                                                                                                             Novel isolated canine or feline TNF-related apoptosis-inducing polypeptide, useful for diagnostic evaluation, genetic testing prognosis of angiogenesis-related disorders, such as cancer.
                                                                                                                                                                                                                   31; 151pp; English
                                                                                                                                                                                                                   Disclosure; SEQ ID NO
                                                                WPI; 2004-376043/35
N-PSDB; ADO24775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 201 AA;
                        Rong S;
                     H,
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75 LVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNG 134 ELVIHEKGFYYIYSQTYFRFQ--EEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSC 192 Gарв 2 Length 201; Indels 12; 59.4%; Score 764; DB 8; ilarity 84.2%; Pred. No. 3.3e-66 Conservative 13; Mismatches 13 Query Match Best Local Similarity Matches 144; Conser 135 61 a D а ð δ ਨੇ

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- 2005
 GenCore (c) 1993
         Copyright
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using sw model - protein search, OM protein

Search time 139 Seconds (without alignments) 604.318 Million cell updat •• 06:44:02 2005, 'n June eno ::

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243

.NEHLIDMDHEASFFGAFLVG 281 US-10-662-431-2_COPY_39_ TNELKQMQDKYSKSGIACFL. score: Sequence: Title: Perfect

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residues 1465611 segs, 345679903 Searched

944584 of hits satisfying chosen parameters: number Total

Minimum

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Database

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*

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No. is the number of results predicted by chance to have greater than or equal to the score of the result being proderived by analysis of the total score distribution. Pred. No. and is score

SUMMARIES

		Description	9-4 Sequence 4,	A-10 Sequence 10, Appl	-14 Sequence 14	-16 Sequence 16,		7-29 Sequence 29,	۲,	-11	9-11 Sequence 11,	1-11 Sequence 11,	-10 Seguence 10,	A-16 Sequence 16,	A-14 Sequence 14, Appl
COLTANATION	;	ID		US-09-900-530	US-10-981-989	US-09-779-050A	US-10-116-37	US-10-959-53	10-216-0	US-10-338-083	US-10-611-39	US-10-794-75	US-10-778-890	US-09-855-544	US-09-855-544
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9-779-050A-1 10-286-696-1 19-855-544A-1 10-855-544A-1 10-652-244-4	5 US-10-399-018-2 US-09-855-544A-9 4 US-10-286-696-1 5 US-10-338-785A- 6 US-10-611-363-2 4 US-10-050-902-2 4 US-10-050-898-2	US-10-289-456- US-10-338-083- US-10-611-399- US-10-794-751- US-10-289-456- US-09-933-915A US-10-289-456- US-09-779-050A-	1 US-09-933-915A- 5 US-10-289-456-1 1 US-09-933-915A- 1 US-09-933-915A- 5 US-10-289-456-8 5 US-10-289-456-1 1 US-09-933-915A- 4 US-10-050-898-3 6 US-10-050-898-3 6 US-10-289-456-1	
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      Sequence 4, Application US/1085559
; Sequence 4, Application US/1085559
; Publication No. US20050031593A1
; GENERAL INFORMATION:
    APPLICANT: Harding, Thomas
    APPLICANT: Lalani, Alshad
; APPLICANT: Donahue, Brian
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery
; TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes
; FILE REFERENCE: 3802-094-27
; CURRENT FILING DATE: 2004-05-28
; FILE REFERENCE: 3802-094-27
; CURRENT FILING DATE: 2003-06-03
; RIMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
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Pred. No. 2.3e-74;
5; Mismatches 13;
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ilarity 85.7%;
Conservative
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Best Local Similarity
Matches 174; Conser
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                                  76 VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
                                                      VRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGE
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 Indel
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APPLICANT: Goddard, Austin
APPLICANT: Gurney, Austin
APPLICANT: Marsters, Scot A.
APPLICANT: Pitti, Robert M.
APPLICANT: Pitti, Robert M.
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US
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Batent No. US200zore

GENERAL INFORMATION:

APPLICANT: BOYLE, WILLIAM

APPLICANT: HSU, HAILING

TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY

FILE REFERENCE: A-570B

CURRENT APPLICATION NUMBER: US/09/779,050A

CURRENT FILING DATE: 2001-02-12

PRIOR APPLICATION NUMBER: 60/181,800

PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/10116378; Publication No. US20020150993A1; GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey, APPLICANT: Gurney, Austin, APPLICANT: Pitti, Robert M.
APPLICANT: Pitti, Robert M.
APPLICANT: Wood, William
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 Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 166; Conser
                                                                                                                                                                                                                                                                           -09-779-050A-16
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US-10-116-378-29
168;
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                   146 NTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFV
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NTKNDKOMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFV
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                                                                                                                                                                                                                                     APPLICANT: Seol, Dae-Wu
APPLICANT: Seol, Dae-Wu
APPLICANT: Billiar, Timothy R.

TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins,
TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus V
TITLE OF INVENTION: Combination and Use in Gene Therapy
FILE REFERENCE: 5006-1-002
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Devi, Gayathri
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Method and Antisense Compound for Potentiating
FILE REFERENCE: 50450.8058.US00
CURRENT APPLICATION NUMBER: US/10/981,989
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/518,139
PRIOR FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARN
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5.1e-74;
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Pred. No. 5.1e-74;
0; Mismatches 0;
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Pred. No.
                                                                   243
                                                                                                                                                                                      Sequence 10, Application US/09900530A Patent No. US20020128438A1
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Publication No. US20050113328A1
GENERAL INFORMATION:
                                                                                     SVTNEHLIDMDHEASFFGAFLVG
                                                                   SVINEHLIDMDHEASFFGAFLVG
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100.0%; Pr
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100.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Devi,
                                                                                                                                                                       -09-900-530A-10
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US-10-981-989-14
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ENGTH: 168
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                                                                   221
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161
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Jun

Fri

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APPLICANT: Shu, Hong-Bing

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT PILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US/09/565,423

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1
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Sequence 11, Application US/10338083

Publication No. US20030166559A1

GENERAL INFORMATION:

APPLICANT: Desjarlais, John R.

APPLICANT: Desjarlais, John R.

APPLICANT: Desjarlais, John R.

TITLE OF INVENTION: Dominant Negative Proteins and Methods There
FILE REFERENCE: A-71273-2

CURRENT APPLICATION NUMBER: US/10/338,083

CURRENT APPLICATION NUMBER: US 60/345,805

PRIOR FILING DATE: 2002-01-04

PRIOR FILING DATE: 2002-04-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.2
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1.3e-70;
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Pred. No.
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Pred. No. 1.9e-71;
); Mismatches 1;
 1998-02-09
                                                                                                                      Score 859; DB 13;
Pred. No. 1.9e-71;
; Mismatches 1
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US-10-959-537-29
; Sequence 29, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FAC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 1999-02-09
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 31
   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10216074
Publication No. US20030148445A1
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Best Local Similarity 99.4%;
Matches 163; Conservative
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ilarity 99.4%;
Conservative
; PRIOR FILING DATE: EARLIER F.; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29
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US-10-959-537-29
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; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-11
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ENGTH: 158
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APPLICANT: Desjarlais, John R.
APPLICANT: Tansey, Malu Lourdes G.
APPLICANT: Tansey, Malu Lourdes G.
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF FILE REFERENCE: A-71273-3
CURRENT APPLICATION NUMBER: US/10/611,399
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/345,805
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
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APPLICANT: Desjarlais, John R.

APPLICANT: Thomason, Adam Read
APPLICANT: Thomason, Adam Read
APPLICANT: Zhukovsky, Eugene Alexander
TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
FILE REFERENCE: A-72175-1
CURRENT APPLICATION NUMBER: US/10/794,751
CURRENT FILING DATE: 2004-03-05
PRIOR FILING DATE: 2003-01-06
PRIOR FILING DATE: 2003-07
PRIOR FILING DATE: 2003-07
PRIOR FILING DATE: 2003-06-23
PRIOR FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-08
PRIOR FILING DATE: 2003-12-08
                Score 849; DB 16;
Pred. No. 1.6e-70;
0; Mismatches 0;
                                                                                                                                   Sequence 11, Application US/10611399
Publication No. US20040170602A1
GENERAL INFORMATION:
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Publication No. US20050048626A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; F
Matches 161; Conservative 0;
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SOFTWARE: PatentIn version 3.3
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LENGTH: 161
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                                                                                          85 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
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         Length 161
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No. 1.6e-70;
Mismatches
                                         0
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red. No. 3.1e-69;
Mismatches 0;
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Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/10778890

Publication No. US20050112596A1

GENERAL INFORMATION:
APPLICANT: TSCHOPP, JURG

TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WI
FILE REFERENCE: A049 US
CURRENT APPLICATION NUMBER: US/10/778,890

CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: US/09/520,489

PRIOR APPLICATION NUMBER: PCT/US98/19191

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-09-12

NUMBER OF SEQ ID NOS: 16
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Pred. No.
         Score 849;
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                                                                                                                                            Indela
                                                                                                                                                                                                                                                      RESULT 13
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                           2;
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Pred. No. 6.1e-61;
); Mismatches 0;
                                                                                                                      9;
                                                                                                                     Score 826; DB 9
Pred. No. 3e-68;
; Mismatches
             544A
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 208
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nilarity 61.7%;
Conservative (
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ilarity 96.3%;
Conservative
                                                                                   , ORGANISM: Homo sapiens
US-09-855-544A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens -09-855-544A-14
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Best Local Similarity
Matches 150; Conser
                                                                                                                               Best Local Similarity
Matches 156; Conser
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Sequence 12, Application US/10286696
Sequence 12, Application US/10286696
Sublication No. US20030129706A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hsu, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene FF
FILE REFERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/10/286,696
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/147,294
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.4e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               49.4%; Score 636; DB 9;
llarity 71.4%; Pred. No. 9.3e-51;
Conservative 20; Mismatches 22
                                                                                         FAMILY
                                                                                                                           US/09/779,050A
Sequence 17, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAI
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,05
CURRENT FILING DATE: 2001-02-12
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 172
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nes 85; Conservative
                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
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120; Conser
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time : 141 sec
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LENGTH: 85
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Best Local S
Matches 120
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39 US-10-662-431-2_COPY_ 1287 Title:

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243

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residues 74649064 513545 seqs, Searched:

410927 hits satisfying chosen parameters of numberTotal

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length: length: seq seq Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Database

Issued Patents AA:*
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 /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/bcTUS_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/bcTUS_COMB.pep:*
 /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, a derived by analysis of the total score distribution. Pred. No. score gand is

SUMMARIES

ជ	ppl	ppl	٦	, App	Ω	33, A	32, Appl	5	p	4, Appli	4, Appli	31, Appl	13, Appl	10, Appl	12, Appl	8, Appli	, App	14, Appl	, App	18, Appl	, App	175, App	20, Appl	84, Appl	<u></u>	pl	176, App
Description		Sequence	Sequence	Sequence	Sequence	Ð	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	Ś	US-09-565-423-7	US-09-105-343A-8	-569-611C-2	US-09-632-287A-12	-513-999C-7	US-09-569-611C-32	US-08-670-354-4	US-09-320-424-4	US-09-825-563-4	PCT-US96-10895-4	9-611	US-09-632-287A-13	US-09-396-937-10	US-09-396-937-12	US-09-396-937-8	-937-1	US-09-396-937-14	-396-937-2	US-09-396-937-18	9	US-09-254-180C-175	US-08-339-214-20	US-08-339-214-84	US-08-649-100-9	US-08-339-214-6	US-09-254-180C-176
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Length	-	191	183	9	85		N	101	101	101	101		87	173	173	187		188	173	173		186	138	178	179	179	179
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Sequence 18, Appl	equence 5, App	Sequence 5, Appli	വ	Ċμ	Ω	Д	Sequence 8, Appl:	4, App	equence 12, Ap	Sequence 81, App.	App	77, A	80, App	App	Sequence 22, App.	9, App	3, A
US-08-339-214-18	US-08-630-172-5	US-09-375-419-5	US-08-339-214-14	US-08-584-031-17	US-09-934-465-17	US-09-582-450-17	US-09-496-118B-8	US-08-339-214-4	US-08-339-214-12	US-08-339-214-81	US-09-565-423-5	US-09-254-180C-177	US-08-339-214-80	Ť	US-09-286-529-22	US-08-339-214-79	US-08-339-214-83
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137	145	145	179		149		152				_	138	-	139	141		136
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28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                         S.R.
: MEMBER OF THE TNF FAMILY USEFUL
: FOR TREATMENT AND DIAGNOSIS OF DISEASE
S: 12
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                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-2623
                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
Sequence 7, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: FOR TREATMENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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ilarity 99.4%;
Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                        ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity
Matches 176; Conser
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126 67 EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL

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RESULT 4
US-09-569-611C-29
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TELEX:
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                                                    SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMK
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EYGLY
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                                                                                      SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                NG
                                                                                                                                                                                                                APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                     60/132,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE
TITLE OF INVENTION: FOR TREATMENT
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09105343A Patent No. 6207642 GENERAL INFORMATION: APPLICANT: WILEY, S.R.
                                                                                                                                                    RESULT 2
US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-06
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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STREET: 10(
CITY: Abbot
STATE: IL
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
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US-09-565-423-7
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Best Local S
Matches 161
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Patent No. 6720182;
GENERAL INFORMATION:
ITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS;
FILE REFERENCE: 2786-0151P;
CURRENT APPLICATION NUMBER: US/09/569,611C;
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 29;
LENGTH: 169
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No. 7.6e-60
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Pred. No. 1.8e-48
; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 654; DB
Pred. No. 7.6e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNLHLRNGELVIHEKGFYYIYSQTYFRFQEE---
                                                                 AFFLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
             US/09/105,343A
                                                                                                                              35,441
ER: 6048.
                                                                                                              NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
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illarity 68.7%;
Conservative 23
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ilarity 99.0%;
Conservative
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                         12-FEB-1998
                                                                                                                                                                                                                                                  183 amino acids
amino acid
APPLICATION DATA:
                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 183 amino aci
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                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
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             APPLICATION NUMBER FILING DATE: 12-F)
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Best Local Similarity
Matches 125; Conser
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                                         CLASSIFICATION:
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; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; WUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; COUNTRY: USA
;
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1.5e-22;
0;
                                                                                                                                                                              Sequence 32, Application US/09569611C
Patent No. 6720182
GENERAL INFORMATION:
APPLICANT: SAVITZKY et al.
TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
FILE REFERENCE: 2786-0151P
CURRENT APPLICATION NUMBER: US/09/569,611C
CURRENT FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 292; DB Pred. No. 1.5e 1; Mismatches
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SOFTWARE: Patentin Ver. 2.0
LENGTH: 120
TYPE.
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29-JUN-1995
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01-NOV-1995
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25-JUN-1996
                                                                                                          118
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5
SOFTWARE: Microsoft Word, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                             TISTVOEKOONISPLVRERG
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Similarity 98.1%;
52; Conservative
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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; ORGANISM: Hom
US-09-569-611C-32
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Matches 52
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US-09-513-999C-7833

i Sequence 7833, Application US/09513999C

j Patent No. 6783961

i GENERAL INFORMATION:

APPLICANT: Ducalert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins

Patent No. 6783961

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 7833

LENGTH: 121
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   166
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TISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSR
                                                                                                                                                                    the
                                                                                   Patent No. 6521422;
GENERAL INFORMATION:
APPLICANT: Hau, Hailing
APPLICANT: Wooden, Scott K
APPLICANT: Wooden, Scott K
APPLICANT: Boyle, William J
TITLE OF INVENTION: Fhm, A No. 6521422el Member of
FILE REFERENCE: 01017/35550A;
CURRENT APPLICATION NUMBER: US/09/632,287A;
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                 Score 446; DB 4; I
Pred. No. 9.6e-39;
0; Mismatches 0;
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seq VIFTVLLQSLCVA/VT
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                                                                      12, Application US/09632287A
5. 6521422
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100.0%; Pr
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100.0%; Pī
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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80; Conservative
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hes 85; Conser
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LOCATION: -32..-1
OTHER INFORMATION:
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NAME/KEY: UNSURE
                                           SULT 5
-09-632-287A-12
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                                                                                                                                                                                                                                                                                        SEQ ID NO 12
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Matches 80
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APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E

CURRENT APPLICATION NUMBER: US/09/320,424

CURRENT FILING DATE: 1999-05-26

EARLIER APPLICATION NUMBER: 09/190,046

EARLIER FILING DATE: 1998-11-10

EARLIER FILING DATE: 1998-03-26

EARLIER FILING DATE: 1996-06-25

EARLIER FILING DATE: 1996-06-25

EARLIER FILING DATE: 1996-06-25

EARLIER FILING DATE: 1995-11-01

EARLIER FILING DATE: 1995-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that Induces Apoptosis
                                                                                                                                                                                                            Score 291; DB 1; Pred. No. 1.5e-22; ); Mismatches 0;
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; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces AF, FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
2835-B
                                                                                                                                                                                                 22.6%; SCC
100.0%; Pr
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Patent No. 6284236
GENERAL INFORMATION:
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100.0%; Pr
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                  4
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REFERENCE/DOCKET NUMBER:
                                                                                                              : 101 amino acids
amino acid
                                      TELEK: (206) 233-vorz
TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acide
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 52; Conservative
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                 ELECUMANTE: (200)
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52; Conser
                                                                                                                                        ; TOPOLOGY: 11; MOLECULE TYPE: US-08-670-354-4
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US-09-320-424-4
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Best Local S
Matches 52
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporatic STREET: 51 University Street
                                                                                                                                                                                                                                                                                                            Score 291; DB 4;
Pred. No. 1.5e-22;
); Mismatches 0;
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APPLICATION NUMBER: PCT/ITCOCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
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25-JUN-1996
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Kathryn A.

32,172

2835-WO
           PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR FILING DATE: 1995-11-01
PRIOR APPLICATION NUMBER: 08/496,632
09/190,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                   22.6%; Sc.
100.0%; Pi
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5
SOFTWARE: Microsoft Word, V
                                                                                                                                                  1995-06-29
OS: 25
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NAME: Anderson, Kathryn
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amino acid
Y: linear
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52; Conservative
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER:
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NUMBER OF SEQ ID NOS: 2:
SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                        LENGTH: 101
TYPE: PRT
ORGANISM: human
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                                                                                                                                                                                            SCFINAL SEQ ID NO 4
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                                                                                                                                                                                                                                                                              US-09-825-563-4
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Best Local S
Matches 52
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STATE:
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86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: 'HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
                                                                                                               for Down-Regulating Osteoprotegerin Ligand
                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: DNA encoding OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: murine OPGL, residues 158-316 with C;
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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                                         GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulat
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/396,937
               ce 10, Application US/09396937
No. 6645500
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Patent No. 6645500
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 173
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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larity 34.2%;
Conservative 33
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Best Local Similarity
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SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                            ; OTHER INFORM US-09-396-937-10
US-09-396-937-10
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Best Local (
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                Sequence
Patent No
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US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; CURRENT FILING DATE: 105.000-08-03
                                                                                                                                                                                      sequence 31, Application US/09569611C;
Patent No. 6720182;
GENERAL INFORMATION:
TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS;
FILE REFERENCE: 2786-0151P;
CURRENT APPLICATION NUMBER: US/09/569,611C;
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 52;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 31;
LENGTH: 122
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5.4e-18;
hes 14;
            DB 5; I
1.5e-22;
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Pred. No. 2e-22;
0; Mismatches (
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Pred. No. 6.4e-
9; Mismatches
                                               Mismatches
               Score 291;
Pred. No.
  22.6%; Sc.
100.0%; Pr
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100.0%; Pi
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US-08-670-354-2

Sequence 2, Application US/08670354

Patent No. 5763223

GENERAL INFORMATION:
APPLICANT: Reymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Ind
APPLICANT: Reymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Ind
APPLICANT: Reymond G. Goodwin.
TITLE OF INVENTION: Society
CORRESPONDENCE ADDIRESS: 9

CORRESPONDENCE ADDIRESS: 9

CORPUTER: Seattle
STAME: WA

COUNTRY: USA
ZIP: 98101

COMPUTER: Rapple Macintosh
OPERATING SYSTEM: US/08/670,354

FILING DATE: 25-UN-1996

CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/670,354

FILING DATE: 29-UN-1995

CLASSIFICATION NUMBER: US 08/496,632

FILING DATE: 29-UN-1995

CLASSIFICATION NUMBER: US 08/548,368

FILING DATE: 29-UN-1995

CLASSIFICATION NUMBER: US 08/548,368

FILING DATE: 10-NOV-1995

CLASSIFICATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 32,044

TELECOWMUNICATION A35

ATTORNEY/AGENT INFORMATION:
TELECOWMUNICATION A35

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REFERENCE/DOCKET NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 32,172

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REGUENCE CHARACTERISTICS:
LENGTH: 281 amino acids

TYPE: amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: INVENT.
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; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
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Mismatches 0;
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TITLE OF INVENTION: APO-2 LIGAND; FILE REFERENCE: 11669.22US03; CURRENT APPLICATION NUMBER: US/08/584,031A; CURRENT FILING DATE: 1996-01-09; NUMBER OF SEQ ID NOS: 17; SOFTWARE: Patentin Ver. 2.0
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Similarity
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Pred. No. 3.5; Mismatches
                                                                                                                                                                  floppy
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flopp
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; TITLE OF INVENTION: MEMBER OF THE 7
; TITLE OF INVENTION: FOR TREATMENT P
; TITLE OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; STATE: 1L
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11 Similarity 100.0%
281; Conservative
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Sequence 6, Application US/0933593A

Patent No. 6313269

GENERAL INFORMATION:

APPLICANT: DEEN, KEITH C.

APPLICANT: YOUNG, PETER R.

APPLICANT: TOSHAK, AMY K.

APPLICANT: TRUNEH, ALEMSEGED

TITLE OF INVENTION: TR6

FILE REFERENCE: GH-50008-2

CURRENT APPLICATION NUMBER: US/09/33,593A

CURRENT APPLICATION NUMBER: 08/916,625

PRIOR FILING DATE: 1997-08-09

PRIOR FILING DATE: 1997-05-09

PRIOR FILING DATE: 1997-03-14

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 3.5e-149,
Mismatches 0;
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Pred. No. 3.5e-149
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      EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/4
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                  100.0%;
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Best Local Similarity 100.0%;
Matches 281; Conservative (
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Best Local Similarity
                                                                                                        TYPE: PRT
CRGANISM: human
US-09-320-424-2
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
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Pred. No. 3.5e-149;
Mismatches 0;
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US/08/883,086
                                                                                                                                                                    NUMBER INFORMATION:
Caki, Princilla E.
33,207
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                                                                                                                                                                                                           NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                      No. 6171787e
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                             281 amino acids
                                                                                        CURRENT APPLICATION DATA
APPLICATION NUMBER: UK
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100
nes 281; Conservative
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                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TOPOLOGY: linear

MOLECULE TYPE: No.

US-08-883-086-10
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                                                 COMPUTER: IBM COINTER: OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                           amino
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                                                                               SOFTWARE:
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US-09-919-039-118
; Sequence 118, Application US/09919039
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281; Conser
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                                                                                           FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDA
                                            RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-8897
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Pred. No. 3.5e-149;
; Mismatches 0;
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SEE: Legal Services
: 301 Henrietta Street
Kalamazoo
                                                                                                                                                                                                                                                                                            TNF-Related Death Ligand
                                                                                                                                                                                                       US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
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Best Local Similarity 100.0%;
Matches 281; Conservative (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
-157-864-11
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Dis
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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ADDRESSEE:
STREET: 301
CITY: Kalan
STATE: MI
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Pred. No. 3.5e-149;
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Patent No. 6521228

GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induce FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/825,51
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1995-11-01
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
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Christina Yu-Ching
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US-10-011-125A-4
; Sequence 4, Application US/1001112:
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Chi
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Best Local Similarity 100.0%;
Matches 281; Conservative
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                   APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A;
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 281
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Pred. No. 3.5e-149
0; Mismatches 0;
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Pred. No. 3.5
; Mismatches
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APPLICANT: Ashkenazi, Avi J.

APPLICANT: Relley, Robert F.

APPLICANT: Pitti, Robert M.

APPLICANT: Pitti, Robert M.

APPLICANT: Schwall, Ralph H.

TITLE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: P0978P4

CURRENT APPLICATION NUMBER: US/09/582,450

CURRENT FILING DATE: 2001-05-14

PRIOR FILING DATE: 1998-01-15

PRIOR FILING DATE: 1998-01-15

PRIOR FILING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 17
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S-09-582-450-1
Sequence 1, Application US/095824
Patent No. 6740739
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                                                                                                                                                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte
US-09-919-039-118
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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ses 281; Conser
Patent No. 6727066
GENERAL INFORMATION:
6727066
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FNGTH: 281
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Pred. No. 3.5e-149;
Mismatches 0;
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; Patent No. 674668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1
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Seattle
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
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                                                                                                                                          Score 1478; DB 4;
Pred. No. 3.5e-149;
Mismatches 0;
TITLE OF INVENTION: BACTERIAL HOST STRAINS FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
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25-JUN-1996
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29-JUN-1995
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01-NOV-1995
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NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                           100.0%;
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Apple Macintosh
                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 281; Conservative
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PRIOR APPLICATION DATA:
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FILING DATE: 29-JUN
                                                                                                TYPE: PRT ORGANISM: Homo sapiens
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FILING DATE: 01-NCCLASSIFICATION:
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CITY: Sec
STATE: WA
COUNTRY:
ZIP: 981(
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US-10-011-125A-4
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RELATED RECEPTORS
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US-09-072-993C-3
i Sequence 3, Application US/09072993C
j Patent No. 6346388
j GENERAL INFORMATION:
i APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS REL
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072, 993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-29
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3.1e-148;
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Pred. No. 3.5;
Mismatches
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Pred. No.
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SOFTWARE: FastSEQ for Windows Version
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 281; Conservative
            TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                TELEX: 756822
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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LENGTH: 279
TYPE: PRT
ORGANISM: HOMO SAPIENS
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279; Conser
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PCT-US96-10895-2
                                                                                 TYPE: amino TOPOLOGY: li
                        TELEFAX:
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Best Local S
Matches 279
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SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV 120
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SIYQG-------IDMDHEASFFGAFLVG
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Best Local Similarity 85.4%; Pred. No. 1.3e-123;
Matches 240; Conservative 2; Mismatches 5;
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                                                                                                                                                                   RESULT 15
US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARI
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
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US-09-569-611C-30
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